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(54) Title: MU-CONOPEPTIDES

(57) Abstract: The present invention is to μ-conopeptides, derivatives or pharmaceutically acceptable salts thereof. The present invention is further directed to the use of this peptide, derivatives thereof and pharmaceutically acceptable salts thereof for the treatment of disorders associated with voltage-gated sodium channels. Thus, the μ-conopeptides or derivatives are useful as neuromuscular blocking agents, local anesthetic agents, analgesic agents and neuroprotective agents. The μ-conopeptides are also useful for treating neuromuscular disorders. The invention is further directed to nucleic acid sequences encoding the μ-conopeptides and encoding propeptides, as well as the propeptides.

TITLE OF THE INVENTION

MU-CONOPEPTIDES

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] The present application claims benefit under 35 USC §119(e) to U.S. provisional patent applications Serial No. 60/219,619 filed on 21 July 2000, Serial No. 60/245,157 filed on 3 November 2000, Serial No. 60/264,319 filed on 29 January 2001 and Serial No. 60/277,270 filed on 21 March 2001. Each of these applications is incorporated herein by reference.

[0002] This invention was made with Government support under Grant No. PO1 GM48677 awarded by the National Institute of General Medical Sciences, National Institutes of Health, Bethesda, Maryland. The United States Government has certain rights in the invention.

BACKGROUND OF THE INVENTION

[0003] The present invention is to μ-conopeptides, derivatives or pharmaceutically acceptable salts thereof. The present invention is further directed to the use of this peptide, derivatives thereof and pharmaceutically acceptable salts thereof for the treatment of disorders associated with voltage-gated sodium channels. Thus, the μ-conopeptides or derivatives are useful as neuromuscular blocking agents, local anesthetic agents, analgesic agents and neuroprotective agents. The μ-conopeptides are also useful for treating neuromuscular disorders. The invention is further directed to nucleic acid sequences encoding the μ-conopeptides and encoding propeptides, as well as the propeptides.

[0004] The publications and other materials used herein to illuminate the background of the invention, and in particular, cases to provide additional details respecting the practice, are incorporated by reference, and for convenience are referenced in the following text by author and date and are listed alphabetically by author in the appended bibliography.

[0005] *Conus* is a genus of predatory marine gastropods (snails) which envenomate their prey. Venomous cone snails use a highly developed projectile apparatus to deliver their cocktail of toxic conotoxins into their prey. In fish-eating species such as *Conus magus* the cone detects the presence of the fish using chemosensors in its siphon and when close enough extends its proboscis and fires a hollow harpoon-like tooth containing venom into the fish. This immobilizes the fish and enables the cone snail to wind it into its mouth via an attached filament. For general information on *Conus* and their venom see the website address

http://grimwade.biochem.unimelb.edu.au/cone/referenc.html. Prey capture is accomplished through a sophisticated arsenal of peptides which target specific ion channel and receptor subtypes. Each *Conus* species venom appears to contain a unique set of 50-200 peptides. The composition of the venom differs greatly between species and between individual snails within each species, each optimally evolved to paralyse it's prey. The active components of the venom are small peptides toxins, typically 10-40 amino acid residues in length and are typically highly constrained peptides due to their high density of disulphide bonds.

[0006] The venoms consist of a large number of different peptide components that when separated exhibit a range of biological activities: when injected into mice they elicit a range of physiological responses from shaking to depression. The paralytic components of the venom that have been the focus of recent investigation are the α-, ω- and μ-conotoxins. All of these conotoxins act by preventing neuronal communication, but each targets a different aspect of the process to achieve this. The α-conotoxins target nicotinic ligand gated channels, the μ-conotoxins target the voltage-gated sodium channels and the ω-conotoxins target the voltage-gated calcium channels (Olivera et al., 1985; Olivera et al., 1990). For example a linkage has been established between α-, αA- & ϕ-conotoxins and the nicotinic ligand-gated ion channel; ω-conotoxins and the voltage-gated calcium channel; μ-conotoxins and the voltage-gated sodium channel; δ-conotoxins and the voltage-gated sodium channel; κ-conotoxins and the voltage-gated potassium channel; conantokins and the ligand-gated glutamate (NMDA) channel.

[0007] However, the structure and function of only a small minority of these peptides have been determined to date. For peptides where function has been determined, three classes of targets have been elucidated: voltage-gated ion channels; ligand-gated ion channels, and G-protein-linked receptors.

[0008] *Conus* peptides which target voltage-gated ion channels include those that delay the inactivation of sodium channels, as well as blockers specific for sodium channels, calcium channels and potassium channels. Peptides that target ligand-gated ion channels include antagonists of NMDA and serotonin receptors, as well as competitive and noncompetitive nicotinic receptor antagonists. Peptides which act on G-protein receptors include neurotensin and vasopressin receptor agonists. The unprecedented pharmaceutical selectivity of conotoxins is at least in part defined by a specific disulfide bond frameworks combined with hypervariable amino acids within disulfide loops (for a review see McIntosh et al., 1998).

[0009] There are drugs used in the treatment of pain, which are known in the literature and to the skilled artisan. See, for example, Merck Manual, 16th Ed. (1992). However, there is a demand for more active analgesic agents with diminished side effects and toxicity and which are non-addictive. The ideal analgesic would reduce the awareness of pain, produce analgesia over a wide range of pain types, act satisfactorily whether given orally or parenterally, produce minimal or no side effects, be free from tendency to produce tolerance and drug dependence.

[0010] Due to the high potency and exquisite selectivity of the conopeptides, several are in various stages of clinical development for treatment of human disorders. For example, two *Conus* peptides are being developed for the treatment of pain. The most advanced is ω-conotoxin MVIIA (ziconotide), an N-type calcium channel blocker (see Heading, C., 1999; U.S. Patent No. 5,859,186). ω-Conotoxin MVIIA, isolated from *Conus magus*, is approximately 1000 times more potent than morphine, yet does not produce the tolerance or addictive properties of opiates. ω-Conotoxin MVIIA has completed Phase III (final stages) of human clinical trials and has been approved as a therapeutic agent. ω-Conotoxin MVIIA is introduced into human patients by means of an implantable, programmable pump with a catheter threaded into the intrathecal space. Preclinical testing for use in post-surgical pain is being carried out on another *Conus* peptide, contulakin-G, isolated from *Conus geographus* (Craig et al. 1999). Contulakin-G is a 16 amino acid O-linked glycopeptide whose C-terminus resembles neurotensin. It is an agonist of neurotensin receptors, but appears significantly more potent than neurotensin in inhibiting pain in *in vivo* assays.

[0011] In view of a large number of biologically active substances in *Conus* species it is desirable to further characterize them and to identify peptides capable of treating disorders involving voltage gated ion channels, such as stroke and pain. Surprisingly, and in accordance with this invention, Applicants have discovered novel conotoxins that can be useful for the treatment of disorders involving voltage gated ion channels and could address a long felt need for a safe and effective treatment.

SUMMARY OF THE INVENTION

[0012] The present invention is to μ-conopeptides, derivatives or pharmaceutically acceptable salts thereof. The present invention is further directed to the use of this peptide, derivatives thereof and pharmaceutically acceptable salts thereof for the treatment of disorders associated with voltage-gated sodium channels. Thus, the μ-conopeptides or derivatives are

useful as neuromuscular blocking agents, local anesthetic agents, analgesic agents and neuroprotective agents. The μ-conopeptides are also useful for treating neuromuscular disorders. The invention is further directed to nucleic acid sequences encoding the μ-conopeptides and encoding propeptides, as well as the propeptides.

[0013] More specifically, the present invention is directed to μ-conopeptides, having the amino acid sequences set forth in Tables 1 and 2 below.

[0014] The present invention is also directed to derivatives or pharmaceutically acceptable salts of the μ-conopeptides or the derivatives. Examples of derivatives include peptides in which the Arg residues may be substituted by Lys, ornithine, homoargine, nor-Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any synthetic basic amino acid; the Lys residues may be substituted by Arg, ornithine, homoargine, nor-Lys, or any synthetic basic amino acid; the Tyr residues may be substituted with meta-Tyr, ortho-Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any synthetic hydroxy containing amino acid; the Ser residues may be substituted with Thr or any synthetic hydroxylated amino acid; the Thr residues may be substituted with Ser or any synthetic hydroxylated amino acid; the Phe residues may be substituted with any synthetic aromatic amino acid; the Trp residues may be substituted with Trp (D), neo-Trp, halo-Trp (D or L) or any aromatic synthetic amino acid; and the Asn, Ser, Thr or Hyp residues may be glycosylated. The halogen may be iodo, chloro, fluoro or bromo; preferably iodo for halogen substituted-Tyr and bromo for halogen-substituted Trp. The Tyr residues may also be substituted with the 3-hydroxyl or 2-hydroxyl isomers (meta-Tyr or ortho-Tyr, respectively) and corresponding O-sulpho- and O-phospho-derivatives. The acidic amino acid residues may be substituted with any synthetic acidic amino acid, e.g., tetrazolyl derivatives of Gly and Ala. The aliphatic amino acids may be substituted by synthetic derivatives bearing non-natural aliphatic branched or linear side chains C_nH_{2n+2} up to and including n=8. The Met residues may be substituted by norleucine (Nle). The Cys residues may be in D or L configuration and may optionally be substituted with homocysteine (D or L).

[0015] Examples of synthetic aromatic amino acid include, but are not limited to, nitro-Phe, 4-substituted-Phe wherein the substituent is C_1-C_3 alkyl, carboxyl, hyrdroxymethyl, sulphomethyl, halo, phenyl, -CHO, -CN, $-SO_3H$ and -NHAc. Examples of synthetic hydroxy containing amino acid, include, but are not limited to, such as 4-hydroxymethyl-Phe, 4-hydroxyphenyl-Gly, 2,6-dimethyl-Tyr and 5-amino-Tyr. Examples of synthetic basic amino acids include, but are not limited to, N-1-(2-pyrazolinyl)-Arg, 2-(4-piperinyl)-Gly, 2-(4-

piperinyl)-Ala, 2-[3-(2S)pyrrolininyl)-Gly and 2-[3-(2S)pyrrolininyl)-Ala. These and other synthetic basic amino acids, synthetic hydroxy containing amino acids or synthetic aromatic amino acids are described in Building Block Index, Version 3.0 (1999 Catalog, pages 4-47 for hydroxy containing amino acids and aromatic amino acids and pages 66-87 for basic amino acids; see also http://www.amino-acids.com), incorporated herein by reference, by and available from RSP Amino Acid Analogues, Inc., Worcester, MA. Examples of synthetic acid amino acids include those derivatives bearing acidic functionality, including carboxyl, phosphate, sulfonate and synthetic tetrazolyl derivatives such as described by Ornstein et al. (1993) and in U.S. Patent No. 5,331,001, each incorporated herein by reference.

[0016] Optionally, in the μ-conopeptides of the present invention, the Asn residues may be modified to contain an N-glycan and the Ser, Thr and Hyp residues may be modified to contain an O-glycan (e.g., g-N, g-S, g-T and g-Hyp). In accordance with the present invention, a glycan shall mean any N-, S- or O-linked mono-, di-, tri-, poly- or oligosaccharide that can be attached to any hydroxy, amino or thiol group of natural or modified amino acids by synthetic or enzymatic methodologies known in the art. The monosaccharides making up the glycan can include D-allose, D-altrose, D-glucose, D-mannose, D-gulose, D-idose, D-galactose, D-talose, D-galactosamine, D-glucosamine, D-N-acetyl-glucosamine (GlcNAc), D-N-acetyl-galactosamine (GalNAc), D-fucose or D-arabinose. These saccharides may be structurally modified, e.g., with one or more O-sulfate, O-phosphate, O-acetyl or acidic groups, such as sialic acid, including combinations thereof. The gylcan may also include similar polyhydroxy groups, such as D-penicillamine 2,5 and halogenated derivatives thereof or polypropylene glycol derivatives. The glycosidic linkage is beta and 1-4 or 1-3, preferably 1-3. The linkage between the glycan and the amino acid may be alpha or beta, preferably alpha and is 1-.

[0017] Core O-glycans have been described by Van de Steen et al. (1998), incorporated herein by reference. Mucin type O-linked oligosaccharides are attached to Ser or Thr (or other hydroxylated residues of the present peptides) by a GalNAc residue. The monosaccharide building blocks and the linkage attached to this first GalNAc residue define the "core glycans," of which eight have been identified. The type of glycosidic linkage (orientation and connectivities) are defined for each core glycan. Suitable glycans and glycan analogs are described further in U.S. Serial No. 09/420,797 filed 19 October 1999 and in PCT Application No. PCT/US99/24380 filed 19 October 1999 (PCT Published Application No. WO 00/23092), each incorporated herein by reference. A preferred glycan is Gal(β1$\rightarrow$3)GalNAc(α1$\rightarrow$).

[0018] Optionally, in the μ-conopeptides described above, pairs of Cys residues may be replaced pairwise with isoteric lactam or ester-thioether replacements, such as Ser/(Glu or Asp), Lys/(Glu or Asp), Cys/(Glu or Asp) or Cys/Ala combinations. Sequential coupling by known methods (Barnay et al., 2000; Hruby et al., 1994; Bitan et al., 1997) allows replacement of native Cys bridges with lactam bridges. Thioether analogs may be readily synthesized using halo-Ala residues commercially available from RSP Amino Acid Analogues.

[0019] The present invention is further directed to derivatives of the above peptides and peptide derivatives which are acylic permutations in which the cyclic permutants retain the native bridging pattern of native toxin. See, for example, Craik et al. (2001).

[0020] The present invention is further directed to a method of treating disorders associated with voltage gated ion channel disorders in a subject comprising administering to the subject an effective amount of the pharmaceutical composition comprising a therapeutically effective amount of a μ-conopeptide described herein or a pharmaceutically acceptable salt or solvate thereof. The present invention is also directed to a pharmaceutical composition comprising a therapeutically effective amount of a μ-conopeptide described herein or a pharmaceutically acceptable salt or solvate thereof and a pharmaceutically acceptable carrier.

[0021] More specifically, the present invention is further directed to uses of these peptides or nucleic acids as described herein as neuromuscular blocking agents, local anesthetic agents, analgesic agents and neuroprotective agents. The μ-conopeptides are also useful for treating neuromuscular disorders.

[0022] The present invention is directed to the use of μ-conopeptides as a local anesthetic for treating pain. The μ-conopeptides have long lasting anesthetic activity and are particularly useful for spinal anesthesia, either administered acutely for post-operative pain or via an intrathecal pump for severe chronic pain situations. The μ-conopeptides are also useful as analgesics in chronic and neuropathic pain states, such as trigeminal neuralgia, diabetic neuropathy, post-herpetic neuralgia, neuroma pain and phantom limb pain. The μ-conopeptides are also useful for treating burn pain and as ocular anesthetics.

[0023] The present invention is directed to the use of μ-conopeptides as neuroprotectants. The μ-conopeptides are useful for the treatment and alleviation of epilepsy and as a general anticonvulsant agent. The μ-conopeptides are also useful for treating neurodegenerative diseases, such as Amyotrophic Lateral Sclerosis (ALS). The μ-conopeptides are further useful as cerebroprotectants, such as for reducing neurotoxic injury associated with

conditions of hypoxia, anoxia or ischemia which typically follows stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, drowning, suffocation, perinatal asphyxia, or hypoglycemic events.

[0024] The present invention is directed to the use of μ-conopeptides as neuromuscular blockers and for treating neuromuscular disorders. As such, the μ-conopeptides are useful for providing relaxation of muscle, for treating benign essential blepharospasm and other forms of focal dystonia and for anti-wrinkle use.

[0025] More specifically, the present invention is also directed to nucleic acids which encode μ-conopeptides of the present invention or which encodes precursor peptides for these μ-conopeptides, as well as the precursor peptide. The nucleic acid sequences encoding the precursor peptides of other μ-conopeptides of the present invention are set forth in Table 1. Table 1 also sets forth the amino acid sequences of these precursor peptides.

[0026] The present invention is further directed to the use of selectively radioiodinated or radiotritiated μ-conopeptides for characterizing pore occlusion sites on different sodium channel subtypes or for use in screening assays.

[0027] The present invention is also directed to the use of μ-conopeptides for screening small molecule libraries to identify small molecules that are selective blocking agents at specific sodium channel subtypes expressed in mammalian systems. In one embodiment, the blocking activity of a small molecule at a particular sodium channel subtype is compared to the blocking activity of a μ-conopeptide at the same sodium channel subtype. In a second embodiment, the ability of a small molecule to displace a μ-conopeptide from a sodium channel subtype is determined. In a third emdiment, the binding affinity of a small molecule for a sodium channel subtype is compared to the binding affinity of a μ-conopeptide for the same sodium channel subtype.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENT

[0028] The present invention is to μ-conopeptides, derivatives or pharmaceutically acceptable salts thereof. The present invention is further directed to the use of this peptide, derivatives thereof and pharmaceutically acceptable salts thereof for the treatment of disorders associated with voltage-gated sodium channels. Thus, the μ-conopeptides or derivatives are useful as neuromuscular blocking agents, local anesthetic agents, analgesic agents and neuroprotective agents. The μ-conopeptides are also useful for treating neuromuscular

disorders. The invention is further directed to nucleic acid sequences encoding the μ-conopeptides and encoding propeptides, as well as the propeptides.

[0029] The present invention, in another aspect, relates to a pharmaceutical composition comprising an effective amount of an μ-conopeptides, a mutein thereof, an analog thereof, an active fragment thereof or pharmaceutically acceptable salts or solvates. Such a pharmaceutical composition has the capability of acting at voltage gated ion channels, and are thus useful for treating a disorder or disease of a living animal body, including a human, which disorder or disease is responsive to the partial or complete blockade of voltage gated ion channels of the central nervous system comprising the step of administering to such a living animal body, including a human, in need thereof a therapeutically effective amount of a pharmaceutical composition of the present invention.

[0030] The present invention is directed to the use of μ-conopeptides as neuromuscular blockers and for treating neuromuscular disorders. As such, the μ-conopeptides are useful for providing relaxation of muscle, for treating benign essential blepharospasm and other forms of focal dystonia and for anti-wrinkle use. Thus, in one aspect, the μ-conopeptides are useful as neurmuscular blocking agents in conjunction with surgery or for intubation of the trachea by conventional parenteral administration e.g., intramuscular or intravenous administration in solution. In a second aspect, the μ-conopeptides are useful as agents for treating neuromuscular disorders such as myofacial pain syndrome, chronic muscle spasm, dystonias and spasticity.

[0031] The primary factor detrimental to neurons in neurological disorders associated with deficient oxygen supply or mitochondrial dysfunction is insufficient ATP production relative to their requirement. As a large part of the energy consumed by brain cells is used for maintenance of the Na^+ gradient across the cellular membrane, reduction of energy demand by down-modulation of voltage-gated Na(+)-channels is one strategy for neuroprotection. In addition, preservation of the inward Na^+ gradient may be beneficial because it is an essential driving force for vital ion exchanges and transport mechanisms such as Ca^{2+} homeostasis and neurotransmitter uptake. Thus, the μ-conopeptides of the present invention are useful as neuroprotectants.

[0032] Thus, the pharmaceutical compositions of the present invention are useful as neuroprotectants, especially cerebroprotectants, neuromuscular blockers, analgesics (both as a local anesthetic and for general analgesia use) or adjuvants to general anesthetics. A "neurological disorder or disease" is a disorder or disease of the nervous system including, but

not limited to, global and focal ischemic and hemorrhagic stroke, head trauma, spinal cord injury, hypoxia-induced nerve cell damage as in cardiac arrest or neonatal distress or epilepsy. In addition, a "neurological disorder or disease" is a disease state and condition in which a neuroprotectant, anticonvulsant, analgesic and/or as an adjunct in general anesthesia may be indicated, useful, recommended or prescribed.

[0033] More specifically, the present invention is directed to the use of these compounds for reducing neurotoxic injury associated with conditions of hypoxia, anoxia or ischemia which typically follows stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, drowning, suffocation, perinatal asphyxia, or hypoglycemic events. The present invention is further directed to the use of these compounds for treating pain, including acute and chronic pain, such migraine, nociceptive and neuropathic pain.

[0034] A "neuroprotectant" is a compound capable of preventing the neuronal death associated with a neurological disorder or disease. An "analgesic" is a compound capable of relieving pain by altering perception of nociceptive stimuli without producing anesthesia or loss of consciousness. A "muscle relaxant" is a compound that reduces muscular tension. An "adjunct in general anesthesia" is a compound useful in conjunction with anesthetic agents in producing the loss of ability to perceive pain associated with the loss of consciousness.

[0035] The invention relates as well to methods useful for treatment of neurological disorders and diseases, including, but not limited to, global and focal ischemic and hemorrhagic stroke, head trauma, spinal cord injury, hypoxia-induced nerve cell damage such as in cardiac arrest or neonatal distress, epilepsy or other convulsive disorders without undesirable side effects.

[0036] Thus, in one embodiment, the invention provides a method of reducing/alleviating/ decreasing the perception of pain by a subject or for inducing analgesia in a subject comprising administering to the subject an effective amount of the pharmaceutical composition comprising a therapeutically effective amount of a μ-conopeptide described herein or a pharmaceutically acceptable salt or solvate thereof. The pain may be acute, persistent, inflammatory or neuropathic pain. The μ-conopeptides are useful as an analgesia for chronic and neuropathic pain states, such as trigeminal neuralgia, diabetic neuropathy, post-herpetic neuralgia, neuroma pain, phantom limb pain. These peptides are also useful for treating burn pain and as ocular anesthetics.

[0037] In a second embodiment, the invention provides a method of reducing/alleviating/ decreasing the perception of pain by a subject or for inducing analgesia, particularly local analgesia, in a subject comprising administering to the subject an effective amount of the pharmaceutical composition comprising a therapeutically effective amount of a μ-conopeptide described herein or a pharmaceutically acceptable salt or solvate thereof. These peptides are also useful for treating burn pain and as ocular anesthetics.

[0038] In a third embodiment, the invention provides a method of treating stroke, head or spinal cord trauma or injury, anoxia, hypoxia-induced nerve cell damage, ischemia, migraine, psychosis, anxiety, schizophrenia, inflammation, movement disorder, epilepsy, any other convulsive disorder or in the prevention of the degenerative changes connected with the same in a subject comprising administering to the subject an effective amount of the pharmaceutical composition comprising a therapeutically effective amount of a μ-conopeptide described herein or a pharmaceutically acceptable salt or solvate thereof.

[0039] In a fourth embodiment, the invention provides a method for providing a neuromuscular block or for treating neuromuscular disorders, such as methods for providing relaxation of muscle, for treating benign essential blepharospasm and other forms of focal dystonia and for anti-wrinkle use. Thus, in one aspect, the μ-conopeptides are useful as neurmuscular blocking agents in conjunction with surgery or for intubation of the trachea by conventional parenteral administration e.g., intramuscular or intravenous administration in solution. In a second aspect, the μ-conopeptides are useful as agents for treating neuromuscular disorders such as myofacial pain syndrome, chronic muscle spasm, dystonias and spasticity.

[0040] The present invention is also directed to the use of μ-conopeptides for screening small molecule libraries to identify small molecules that are selective blocking agents at specific sodium channel subtypes expressed in mammalian systems. In one embodiment, the blocking activity of a small molecule at a particular sodium channel subtype is compared to the blocking activity of a μ-conopeptide at the same sodium channel subtype. In a second embodiment, the ability of a small molecule to displace a μ-conopeptide from a sodium channel subtype is determined. In a third emdiment, the binding affinity of a small molecule for a sodium channel subtype is compared to the binding affinity of a μ-conopeptide for the same sodium channel subtype.

[0041] The μ-conopeptides described herein are sufficiently small to be chemically synthesized. General chemical syntheses for preparing the foregoing ω-conotoxin peptides are

described hereinafter. Various ones of the μ-conopeptides can also be obtained by isolation and purification from specific *Conus* species using the technique described in U.S. Patent Nos. 4,447,356 (Olivera et al., 1984); 5,514,774; 5,719,264; and 5,591,821, as well as in PCT published application WO 98/03189, the disclosures of which are incorporated herein by reference.

[0042] Although the μ-conopeptides of the present invention can be obtained by purification from cone snails, because the amounts of μ-conopeptides obtainable from individual snails are very small, the desired substantially pure μ-conopeptides are best practically obtained in commercially valuable amounts by chemical synthesis using solid-phase strategy. For example, the yield from a single cone snail may be about 10 micrograms or less of μ-conopeptides peptide. By "substantially pure" is meant that the peptide is present in the substantial absence of other biological molecules of the same type; it is preferably present in an amount of at least about 85% purity and preferably at least about 95% purity. Chemical synthesis of biologically active μ-conopeptides peptides depends of course upon correct determination of the amino acid sequence.

[0043] The μ-conopeptides can also be produced by recombinant DNA techniques well known in the art. Such techniques are described by Sambrook et al. (1989). A gene of interest (i.e., a gene that encodes a suitable μ-conopeptides) can be inserted into a cloning site of a suitable expression vector by using standard techniques. These techniques are well known to those skilled in the art. The expression vector containing the gene of interest may then be used to transfect the desired cell line. Standard transfection techniques such as calcium phosphate co-precipitation, DEAE-dextran transfection or electroporation may be utilized. A wide variety of host/expression vector combinations may be used to express a gene encoding a conotoxin peptide of interest. Such combinations are well known to a skilled artisan. The peptides produced in this manner are isolated, reduced if necessary, and oxidized to form the correct disulfide bonds.

[0044] One method of forming disulfide bonds in the μ-conopeptides of the present invention is the air oxidation of the linear peptides for prolonged periods under cold room temperatures or at room temperature. This procedure results in the creation of a substantial amount of the bioactive, disulfide-linked peptides. The oxidized peptides are fractionated using reverse-phase high performance liquid chromatography (HPLC) or the like, to separate peptides having different linked configurations. Thereafter, either by comparing these fractions with the

elution of the native material or by using a simple assay, the particular fraction having the correct linkage for maximum biological potency is easily determined. However, because of the dilution resulting from the presence of other fractions of less biopotency, a somewhat higher dosage may be required.

[0045] The peptides are synthesized by a suitable method, such as by exclusively solid-phase techniques, by partial solid-phase techniques, by fragment condensation or by classical solution couplings.

[0046] In conventional solution phase peptide synthesis, the peptide chain can be prepared by a series of coupling reactions in which constituent amino acids are added to the growing peptide chain in the desired sequence. Use of various coupling reagents, e.g., dicyclohexylcarbodiimide or diisopropylcarbonyldimidazole, various active esters, e.g., esters of N-hydroxyphthalimide or N-hydroxy-succinimide, and the various cleavage reagents, to carry out reaction in solution, with subsequent isolation and purification of intermediates, is well known classical peptide methodology. Classical solution synthesis is described in detail in the treatise, "Methoden der Organischen Chemie (Houben-Weyl): Synthese von Peptiden," (1974). Techniques of exclusively solid-phase synthesis are set forth in the textbook, "Solid-Phase Peptide Synthesis," (Stewart and Young, 1969), and are exemplified by the disclosure of U.S. Patent 4,105,603 (Vale et al., 1978). The fragment condensation method of synthesis is exemplified in U.S. Patent 3,972,859 (1976). Other available syntheses are exemplified by U.S. Patents No. 3,842,067 (1974) and 3,862,925 (1975). The synthesis of peptides containing γ-carboxyglutamic acid residues is exemplified by Rivier et al. (1987), Nishiuchi et al. (1993) and Zhou et al. (1996).

[0047] Common to such chemical syntheses is the protection of the labile side chain groups of the various amino acid moieties with suitable protecting groups which will prevent a chemical reaction from occurring at that site until the group is ultimately removed. Usually also common is the protection of an α-amino group on an amino acid or a fragment while that entity reacts at the carboxyl group, followed by the selective removal of the α-amino protecting group to allow subsequent reaction to take place at that location. Accordingly, it is common that, as a step in such a synthesis, an intermediate compound is produced which includes each of the amino acid residues located in its desired sequence in the peptide chain with appropriate side-chain protecting groups linked to various ones of the residues having labile side chains.

[0048] As far as the selection of a side chain amino protecting group is concerned, generally one is chosen which is not removed during deprotection of the α-amino groups during the synthesis. However, for some amino acids, e.g., His, protection is not generally necessary. In selecting a particular side chain protecting group to be used in the synthesis of the peptides, the following general rules are followed: (a) the protecting group preferably retains its protecting properties and is not split off under coupling conditions, (b) the protecting group should be stable under the reaction conditions selected for removing the α-amino protecting group at each step of the synthesis, and (c) the side chain protecting group must be removable, upon the completion of the synthesis containing the desired amino acid sequence, under reaction conditions that will not undesirably alter the peptide chain.

[0049] It should be possible to prepare many, or even all, of these peptides using recombinant DNA technology. However, when peptides are not so prepared, they are preferably prepared using the Merrifield solid-phase synthesis, although other equivalent chemical syntheses known in the art can also be used as previously mentioned. Solid-phase synthesis is commenced from the C-terminus of the peptide by coupling a protected α-amino acid to a suitable resin. Such a starting material can be prepared by attaching an α-amino-protected amino acid by an ester linkage to a chloromethylated resin or a hydroxymethyl resin, or by an amide bond to a benzhydrylamine (BHA) resin or paramethylbenzhydrylamine (MBHA) resin. Preparation of the hydroxymethyl resin is described by Bodansky et al. (1966). Chloromethylated resins are commercially available from Bio Rad Laboratories (Richmond, CA) and from Lab. Systems, Inc. The preparation of such a resin is described by Stewart and Young (1969). BHA and MBHA resin supports are commercially available, and are generally used when the desired polypeptide being synthesized has an unsubstituted amide at the C-terminus. Thus, solid resin supports may be any of those known in the art, such as one having the formulae -O-CH_2-resin support, -NH BHA resin support, or -NH-MBHA resin support. When the unsubstituted amide is desired, use of a BHA or MBHA resin is preferred, because cleavage directly gives the amide. In case the N-methyl amide is desired, it can be generated from an N-methyl BHA resin. Should other substituted amides be desired, the teaching of U.S. Patent No. 4,569,967 (Kornreich et al., 1986) can be used, or should still other groups than the free acid be desired at the C-terminus, it may be preferable to synthesize the peptide using classical methods as set forth in the Houben-Weyl text (1974).

[0050] The C-terminal amino acid, protected by Boc or Fmoc and by a side-chain protecting group, if appropriate, can be first coupled to a chloromethylated resin according to the procedure set forth in K. Horiki et al. (1978), using KF in DMF at about 60°C for 24 hours with stirring, when a peptide having free acid at the C-terminus is to be synthesized. Following the coupling of the BOC-protected amino acid to the resin support, the α-amino protecting group is removed, as by using trifluoroacetic acid (TFA) in methylene chloride or TFA alone. The deprotection is carried out at a temperature between about 0°C and room temperature. Other standard cleaving reagents, such as HCl in dioxane, and conditions for removal of specific α-amino protecting groups may be used as described in Schroder & Lubke (1965).

[0051] After removal of the α-amino-protecting group, the remaining α-amino- and side chain-protected amino acids are coupled step-wise in the desired order to obtain the intermediate compound defined hereinbefore, or as an alternative to adding each amino acid separately in the synthesis, some of them may be coupled to one another prior to addition to the solid phase reactor. Selection of an appropriate coupling reagent is within the skill of the art. Particularly suitable as a coupling reagent is N,N'-dicyclohexylcarbodiimide (DCC, DIC, HBTU, HATU, TBTU in the presence of HoBt or HoAt).

[0052] The activating reagents used in the solid phase synthesis of the peptides are well known in the peptide art. Examples of suitable activating reagents are carbodiimides, such as N,N'-diisopropylcarbodiimide and N-ethyl-N'-(3-dimethylaminopropyl)carbodiimide. Other activating reagents and their use in peptide coupling are described by Schroder & Lubke (1965) and Kapoor (1970).

[0053] Each protected amino acid or amino acid sequence is introduced into the solid-phase reactor in about a twofold or more excess, and the coupling may be carried out in a medium of dimethylformamide (DMF):CH_2Cl_2 (1:1) or in DMF or CH_2Cl_2 alone. In cases where intermediate coupling occurs, the coupling procedure is repeated before removal of the α-amino protecting group prior to the coupling of the next amino acid. The success of the coupling reaction at each stage of the synthesis, if performed manually, is preferably monitored by the ninhydrin reaction, as described by Kaiser et al. (1970). Coupling reactions can be performed automatically, as on a Beckman 990 automatic synthesizer, using a program such as that reported in Rivier et al. (1978).

[0054] After the desired amino acid sequence has been completed, the intermediate peptide can be removed from the resin support by treatment with a reagent, such as liquid

hydrogen fluoride or TFA (if using Fmoc chemistry), which not only cleaves the peptide from the resin but also cleaves all remaining side chain protecting groups and also the -amino protecting group at the N-terminus if it was not previously removed to obtain the peptide in the form of the free acid. If Met is present in the sequence, the Boc protecting group is preferably first removed using trifluoroacetic acid (TFA)/ethanedithiol prior to cleaving the peptide from the resin with HF to eliminate potential S-alkylation. When using hydrogen fluoride or TFA for cleaving, one or more scavengers such as anisole, cresol, dimethyl sulfide and methylethyl sulfide are included in the reaction vessel.

[0055] Cyclization of the linear peptide is preferably affected, as opposed to cyclizing the peptide while a part of the peptido-resin, to create bonds between Cys residues. To effect such a disulfide cyclizing linkage, fully protected peptide can be cleaved from a hydroxymethylated resin or a chloromethylated resin support by ammonolysis, as is well known in the art, to yield the fully protected amide intermediate, which is thereafter suitably cyclized and deprotected. Alternatively, deprotection, as well as cleavage of the peptide from the above resins or a benzhydrylamine (BHA) resin or a methylbenzhydrylamine (MBHA), can take place at 0°C with hydrofluoric acid (HF) or TFA, followed by oxidation as described above.

[0056] The peptides are also synthesized using an automatic synthesizer. Amino acids are sequentially coupled to an MBHA Rink resin (typically 100 mg of resin) beginning at the C-terminus using an Advanced Chemtech 357 Automatic Peptide Synthesizer. Couplings are carried out using 1,3-diisopropylcarbodimide in N-methylpyrrolidinone (NMP) or by 2-(1H-benzotriazole-1-yl)-1,1,3,3-tetramethyluronium hexafluorophosphate (HBTU) and diethylisopropylethylamine (DIEA). The FMOC protecting group is removed by treatment with a 20% solution of piperidine in dimethylformamide(DMF). Resins are subsequently washed with DMF (twice), followed by methanol and NMP.

[0057] Muteins, analogs or active fragments, of the foregoing conotoxin peptides are also contemplated here. See, e.g., Hammerland et al. (1992). Derivative muteins, analogs or active fragments of the conotoxin peptides may be synthesized according to known techniques, including conservative amino acid substitutions, such as outlined in U.S. Patent Nos. 5,545,723 (see particularly col. 2, line 50--col. 3, line 8); 5,534,615 (see particularly col. 19, line 45--col. 22, line 33); and 5,364,769 (see particularly col. 4, line 55--col. 7, line 26), each herein incorporated by reference.

[0058] The μ-conopeptides of the present invention are also useful to reduce neurotoxic injury associated with conditions of hypoxia, anoxia or ischemia which typically follows stroke, cerebrovascular accident, brain or spinal chord trauma, myocardial infarct, physical trauma, drownings, suffocation, perinatal asphyxia, or hypoglycemic events. To reduce neurotoxic injury, an ω-conopeptide should be administered in a therapeutically effective amount to the patient within 24 hours of the onset of the hypoxic, anoxic or ischemic condition in order for the μ-conopeptide to effectively minimize the CNS damage which the patient will experience.

[0059] The μ-conopeptides of the present invention are further useful in controlling pain, e.g., as analgesic agents, and the treatment of migraine, acute pain or persistent pain. They can be used prophylactically or to relieve the symptoms associated with a migraine episode, or to treat acute or persistent pain. For these uses, an μ-conopeptide is administered in a therapeutically effective amount to overcome or to ease the pain.

[0060] The μ-conopeptides of the present invention are also useful as neuromuscular blockers and for treating neuromuscular disorders. They can be used for providing relaxation of muscle, for treating benign essential blepharospasm and other forms of focal dystonia and for anti-wrinkle use. Thus, in one aspect, the μ-conopeptides are used as neurmuscular blocking agents in conjunction with surgery or for intubation of the trachea by conventional parenteral administration e.g., intramuscular or intravenous administration in solution. In a second aspect, the μ-conopeptides are used as agents for treating neuromuscular disorders such as myofacial pain syndrome, chronic muscle spasm, dystonias and spasticity. For these uses, a μ-conopeptide is administered in a therapeutically effective amount to relax muscle or provide a neuromuscular block.

[0061] Pharmaceutical compositions containing a compound of the present invention as the active ingredient can be prepared according to conventional pharmaceutical compounding techniques. See, for example, *Remington's Pharmaceutical Sciences*, 18th Ed. (1990, Mack Publishing Co., Easton, PA). Typically, an antagonistic amount of active ingredient will be admixed with a pharmaceutically acceptable carrier. The carrier may take a wide variety of forms depending on the form of preparation desired for administration, e.g., intravenous, oral, parenteral or intrathecally. For examples of delivery methods see U.S. Patent No. 5,844,077, incorporated herein by reference.

[0062] "Pharmaceutical composition" means physically discrete coherent portions suitable for medical administration. "Pharmaceutical composition in dosage unit form" means

physically discrete coherent units suitable for medical administration, each containing a daily dose or a multiple (up to four times) or a sub-multiple (down to a fortieth) of a daily dose of the active compound in association with a carrier and/or enclosed within an envelope. Whether the composition contains a daily dose, or for example, a half, a third or a quarter of a daily dose, will depend on whether the pharmaceutical composition is to be administered once or, for example, twice, three times or four times a day, respectively.

[0063] The term "salt", as used herein, denotes acidic and/or basic salts, formed with inorganic or organic acids and/or bases, preferably basic salts. While pharmaceutically acceptable salts are preferred, particularly when employing the compounds of the invention as medicaments, other salts find utility, for example, in processing these compounds, or where non-medicament-type uses are contemplated. Salts of these compounds may be prepared by art-recognized techniques.

[0064] Examples of such pharmaceutically acceptable salts include, but are not limited to, inorganic and organic addition salts, such as hydrochloride, sulphates, nitrates or phosphates and acetates, trifluoroacetates, propionates, succinates, benzoates, citrates, tartrates, fumarates, maleates, methane-sulfonates, isothionates, theophylline acetates, salicylates, respectively, or the like. Lower alkyl quaternary ammonium salts and the like are suitable, as well.

[0065] As used herein, the term "pharmaceutically acceptable" carrier means a non-toxic, inert solid, semi-solid liquid filler, diluent, encapsulating material, formulation auxiliary of any type, or simply a sterile aqueous medium, such as saline. Some examples of the materials that can serve as pharmaceutically acceptable carriers are sugars, such as lactose, glucose and sucrose, starches such as corn starch and potato starch, cellulose and its derivatives such as sodium carboxymethyl cellulose, ethyl cellulose and cellulose acetate; powdered tragacanth; malt, gelatin, talc; excipients such as cocoa butter and suppository waxes; oils such as peanut oil, cottonseed oil, safflower oil, sesame oil, olive oil, corn oil and soybean oil; glycols, such as propylene glycol, polyols such as glycerin, sorbitol, mannitol and polyethylene glycol; esters such as ethyl oleate and ethyl laurate, agar; buffering agents such as magnesium hydroxide and aluminum hydroxide; alginic acid; pyrogen-free water; isotonic saline, Ringer's solution; ethyl alcohol and phosphate buffer solutions, as well as other non-toxic compatible substances used in pharmaceutical formulations.

[0066] Wetting agents, emulsifiers and lubricants such as sodium lauryl sulfate and magnesium stearate, as well as coloring agents, releasing agents, coating agents, sweetening,

flavoring and perfuming agents, preservatives and antioxidants can also be present in the composition, according to the judgment of the formulator. Examples of pharmaceutically acceptable antioxidants include, but are not limited to, water soluble antioxidants such as ascorbic acid, cysteine hydrochloride, sodium bisulfite, sodium metabisulfite, sodium sulfite, and the like; oil soluble antioxidants, such as ascorbyl palmitate, butylated hydroxyanisole (BHA), butylated hydroxytoluene (BHT), lecithin, propyl gallate, aloha-tocopherol and the like; and the metal chelating agents such as citric acid, ethylenediamine tetraacetic acid (EDTA), sorbitol, tartaric acid, phosphoric acid and the like.

[0067] For oral administration, the compounds can be formulated into solid or liquid preparations such as capsules, pills, tablets, lozenges, melts, powders, suspensions or emulsions. In preparing the compositions in oral dosage form, any of the usual pharmaceutical media may be employed, such as, for example, water, glycols, oils, alcohols, flavoring agents, preservatives, coloring agents, suspending agents, and the like in the case of oral liquid preparations (such as, for example, suspensions, elixirs and solutions); or carriers such as starches, sugars, diluents, granulating agents, lubricants, binders, disintegrating agents and the like in the case of oral solid preparations (such as, for example, powders, capsules and tablets). Because of their ease in administration, tablets and capsules represent the most advantageous oral dosage unit form, in which case solid pharmaceutical carriers are obviously employed. If desired, tablets may be sugar-coated or enteric-coated by standard techniques. The active agent can be encapsulated to make it stable to passage through the gastrointestinal tract while at the same time allowing for passage across the blood brain barrier. See for example, WO 96/11698.

[0068] For parenteral administration, the compound may be dissolved in a pharmaceutical carrier and administered as either a solution or a suspension. Illustrative of suitable carriers are water, saline, dextrose solutions, fructose solutions, ethanol, or oils of animal, vegetative or synthetic origin. The carrier may also contain other ingredients, for example, preservatives, suspending agents, solubilizing agents, buffers and the like. When the compounds are being administered intrathecally, they may also be dissolved in cerebrospinal fluid.

[0069] A variety of administration routes are available. The particular mode selected will depend of course, upon the particular drug selected, the severity of the disease state being treated and the dosage required for therapeutic efficacy. The methods of this invention, generally speaking, may be practiced using any mode of administration that is medically acceptable,

meaning any mode that produces effective levels of the active compounds without causing clinically unacceptable adverse effects. Such modes of administration include oral, rectal, sublingual, topical, nasal, transdermal or parenteral routes. The term "parenteral" includes subcutaneous, intravenous, epidural, irrigation, intramuscular, release pumps, or infusion.

[0070] For example, administration of the active agent according to this invention may be achieved using any suitable delivery means, including:

(a) pump (see, e.g., Luer & Hatton (1993), Zimm et al. (1984) and Ettinger et al. (1978));

(b), microencapsulation (see, e.g., U.S. Patent Nos. 4,352,883; 4,353,888; and 5,084,350);

(c) continuous release polymer implants (see, e.g., U.S. Patent No. 4,883,666);

(d) macroencapsulation (see, e.g., U.S. Patent Nos. 5,284,761, 5,158,881, 4,976,859 and 4,968,733 and published PCT patent applications WO92/19195, WO 95/05452);

(e) naked or unencapsulated cell grafts to the CNS (see, e.g., U.S. Patent Nos. 5,082,670 and 5,618,531);

(f) injection, either subcutaneously, intravenously, intra-arterially, intramuscularly, or to other suitable site; or

(g) oral administration, in capsule, liquid, tablet, pill, or prolonged release formulation.

[0071] In one embodiment of this invention, an active agent is delivered directly into the CNS, preferably to the brain ventricles, brain parenchyma, the intrathecal space or other suitable CNS location, most preferably intrathecally.

[0072] Alternatively, targeting therapies may be used to deliver the active agent more specifically to certain types of cell, by the use of targeting systems such as antibodies or cell specific ligands. Targeting may be desirable for a variety of reasons, e.g. if the agent is unacceptably toxic, or if it would otherwise require too high a dosage, or if it would not otherwise be able to enter the target cells.

[0073] The active agents, which are peptides, can also be administered in a cell based delivery system in which a DNA sequence encoding an active agent is introduced into cells designed for implantation in the body of the patient, especially in the spinal cord region. Suitable delivery systems are described in U.S. Patent No. 5,550,050 and published PCT Application Nos. WO 92/19195, WO 94/25503, WO 95/01203, WO 95/05452, WO 96/02286, WO 96/02646, WO 96/40871, WO 96/40959 and WO 97/12635. Suitable DNA sequences can

be prepared synthetically for each active agent on the basis of the developed sequences and the known genetic code.

[0074] Exemplary methods for administering such muscle relaxant compounds (e.g., so as to achieve sterile or aseptic conditions) will be apparent to the skilled artisan. Certain methods suitable for administering compounds useful according to the present invention are set forth in Goodman and Gilman's *The Pharmacological Basis of Therapeutics*, 7th Ed. (1985). The administration to the patient can be intermittent; or at a gradual, continuous, constant or controlled rate. Administration can be to a warm-blooded animal (e.g. a mammal, such as a mouse, rat, cat, rabbit, dog, pig, cow or monkey); but advantageously is administered to a human being. Administration occurs after general anesthesia is administered. The frequency of administration normally is determined by an anesthesiologist, and typically varies from patient to patient.

[0075] The active agent is preferably administered in an therapeutically effective amount. By a "therapeutically effective amount" or simply "effective amount" of an active compound is meant a sufficient amount of the compound to treat the desired condition at a reasonable benefit/risk ratio applicable to any medical treatment. The actual amount administered, and the rate and time-course of administration, will depend on the nature and severity of the condition being treated. Prescription of treatment, e.g. decisions on dosage, timing, etc., is within the responsibility of general practitioners or spealists, and typically takes account of the disorder to be treated, the condition of the individual patient, the site of delivery, the method of administration and other factors known to practitioners. Examples of techniques and protocols can be found in *Remington's Parmaceutical Sciences*.

[0076] Dosage may be adjusted appropriately to achieve desired drug levels, locally or systemically. Typically the active agents of the present invention exhibit their effect at a dosage range from about 0.001 mg/kg to about 250 mg/kg, preferably from about 0.01 mg/kg to about 100 mg/kg of the active ingredient, more preferably from a bout 0.05 mg/kg to about 75 mg/kg. A suitable dose can be administered in multiple sub-doses per day. Typically, a dose or sub-dose may contain from about 0.1 mg to about 500 mg of the active ingredient per unit dosage form. A more preferred dosage will contain from about 0.5 mg to about 100 mg of active ingredient per unit dosage form. Dosages are generally initiated at lower levels and increased until desired effects are achieved. In the event that the response in a subject is insufficient at such doses, even higher doses (or effective higher doses by a different, more localized delivery

route) may be employed to the extent that patient tolerance permits. Continuous dosing over, for example 24 hours or multiple doses per day are contemplated to achieve appropriate systemic levels of compounds.

[0077] For the treatment of pain, if the route of administration is directly to the CNS, the dosage contemplated is from about 1 ng to about 100 mg per day, preferably from about 100 ng to about 10 mg per day, more preferably from about 1 μg to about 100 μg per day. If administered peripherally, the dosage contemplated is somewhat higher, from about 100 ng to about 1000 mg per day, preferably from about 10 μg to about 100 mg per day, more preferably from about 100 μg to about 10 mg per day. If the conopeptide is delivered by continuous infusion (e.g., by pump delivery, biodegradable polymer delivery or cell-based delivery), then a lower dosage is contemplated than for bolus delivery.

[0078] Advantageously, the compositions are formulated as dosage units, each unit being adapted to supply a fixed dose of active ingredients. Tablets, coated tablets, capsules, ampoules and suppositories are examples of dosage forms according to the invention.

[0079] It is only necessary that the active ingredient constitute an effective amount, i.e., such that a suitable effective dosage will be consistent with the dosage form employed in single or multiple unit doses. The exact individual dosages, as well as daily dosages, are determined according to standard medical principles under the direction of a physician or veterinarian for use humans or animals.

[0080] The pharmaceutical compositions will generally contain from about 0.0001 to 99 wt. %, preferably about 0.001 to 50 wt. %, more preferably about 0.01 to 10 wt.% of the active ingredient by weight of the total composition. In addition to the active agent, the pharmaceutical compositions and medicaments can also contain other pharmaceutically active compounds. Examples of other pharmaceutically active compounds include, but are not limited to, analgesic agents, cytokines and therapeutic agents in all of the major areas of clinical medicine. When used with other pharmaceutically active compounds, the conopeptides of the present invention may be delivered in the form of drug cocktails. A cocktail is a mixture of any one of the compounds useful with this invention with another drug or agent. In this embodiment, a common administration vehicle (e.g., pill, tablet, implant, pump, injectable solution, etc.) would contain both the instant composition in combination supplementary potentiating agent. The individual drugs of the cocktail are each administered in therapeutically effective amounts. A therapeutically effective amount will be determined by the parameters described above; but, in

any event, is that amount which establishes a level of the drugs in the area of body where the drugs are required for a period of time which is effective in attaining the desired effects.

[0081] The practice of the present invention employs, unless otherwise indicated, conventional techniques of chemistry, molecular biology, microbiology, recombinant DNA, genetics, immunology, cell biology, cell culture and transgenic biology, which are within the skill of the art. See, e.g., Maniatis *et al.*, 1982; Sambrook *et al.*, 1989; Ausubel *et al.*, 1992; Glover, 1985; Anand, 1992; Guthrie and Fink, 1991; Harlow and Lane, 1988; Jakoby and Pastan, 1979; *Nucleic Acid Hybridization* (B. D. Hames & S. J. Higgins eds. 1984); *Transcription And Translation* (B. D. Hames & S. J. Higgins eds. 1984); *Culture Of Animal Cells* (R. I. Freshney, Alan R. Liss, Inc., 1987); *Immobilized Cells And Enzymes* (IRL Press, 1986); B. Perbal, *A Practical Guide To Molecular Cloning* (1984); the treatise, *Methods In Enzymology* (Academic Press, Inc., N.Y.); *Gene Transfer Vectors For Mammalian Cells* (J. H. Miller and M. P. Calos eds., 1987, Cold Spring Harbor Laboratory); *Methods In Enzymology*, Vols. 154 and 155 (Wu et al. eds.), *Immunochemical Methods In Cell And Molecular Biology* (Mayer and Walker, eds., Academic Press, London, 1987); *Handbook Of Experimental Immunology*, Volumes I-IV (D. M. Weir and C. C. Blackwell, eds., 1986); Riott, *Essential Immunology*, 6th Edition, Blackwell Scientific Publications, Oxford, 1988; Hogan et al., Manipulating the Mouse Embryo, (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986).

EXAMPLES

[0082] The present invention is described by reference to the following Examples, which are offered by way of illustration and are not intended to limit the invention in any manner. Standard techniques well known in the art or the techniques specifically described below were utilized.

EXAMPLE 1

Isolation of μ-Conopeptides

[0083] Crude venom was extracted from venom ducts (Cruz et al., 1976), and the components were purified as previously described (Cartier et al., 1996). The crude extract from venom ducts was purified by reverse phase liquid chromatography (RPLC) using a Vydac C_{18}

semi-preparative column (10 x 250 mm). Further purification of bioactive peaks was done on a Vydac C_{18} analytical column (4.6 x 220 mm). The effluents were monitored at 220 nm. Peaks were collected, and aliquots were assayed for activity. Throughout purification, HPLC fractions were assayed by means of intracerebral ventricular (i.c.v.) injection into mice (Clark et al., 1981).

[0084] The amino acid sequence of the purified peptides were determined by standard methods. The purified peptides were reduced and alkylated prior to sequencing by automated Edman degradation on an Applied Biosystems 477A Protein Sequencer with a 120A Analyzer (DNA/Peptide Facility, University of Utah) (Martinez et al., 1995; Shon et al., 1994).

[0085] In accordance with this method, the μ-conopeptides described as "isolated" in Table 1 were obtained. These μ-conopeptides, as well as the other μ-conopeptides and the μ-conopeptide precursors set forth in Table 1 are synthesized as described in U.S. Patent No. 5,670,622.

EXAMPLE 2

Isolation of DNA Encoding μ-Conopeptides

[0086] DNA coding for μ-conopeptides was isolated and cloned in accordance with conventional techniques using general procedures well known in the art, such as described in Olivera et al. (1996). Alternatively, cDNA libraries was prepared from *Conus* venom duct using conventional techniques. DNA from single clones was amplified by conventional techniques using primers which correspond approximately to the M13 universal priming site and the M13 reverse universal priming site. Clones having a size of approximately 300-500 nucleotides were sequenced and screened for similarity in sequence to known μ-conotoxins. The DNA sequences and encoded propeptide sequences are set forth in Table 1. DNA sequences coding for the mature toxin can also be prepared on the basis of the DNA sequences set forth in Table1. An alignment of the μ-conopeptides of the present invention is set forth in Table 2.

TABLE 1

DNA and Amino Acid Sequences of μ-Conopeptides and Precursors

Name: Ar3.1
Species: arenatus
Cloned: Yes

DNA Sequence:
CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTCTTGACCATCTG TATGCTTCTGTTTCCCCTTACTGCTCTTCCGCTGGATGGGGATCAACCTGCAGACCG ACCTGCAGAGCGTATGCAGGACGACTTTATAACTGAGCATCATCCCCTGTTTGATCC TGTCAAACGGTGTTGCGAGAGGCCATGCAACATAGGATGCGTACCTTGTTGTTAATG ACCAGCTTTGTCATCGCGGCCTCATCAAGCGAATAAGTAAAACGATTGCAGT (SEQ ID NO:1)

Translation:
MMSKLGVFLTICMLLFPLTALPLDGDQPADRPAERMQDDFITEHHPLFDPVKRCCERPC NIGCVPCC (SEQ ID NO:2)

Toxin Sequence:
Cys-Cys-Xaa1-Arg-Xaa3-Cys-Asn-Ile-Gly-Cys-Val-Xaa3-Cys-Cys-^ (SEQ ID NO:3)

Name: Ak3.1
Species: atlanticus
Cloned: Yes

DNA Sequence:
GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCAC TTACTGCTCTTCCGCTGGATGAAGATCAACCGGTACACCGACCTGCAGAGCGTATGC AGGACATTTCATCTGATCAACATCTCTTCTTTGATCTCATCAAACGGTGCTGCGAGT TGCCATGCGGGCCAGGCTTTTGCGTCCCTTGTTGCTGACATCAATAACGTGTTGATG ACCAACTTTCTCGAG (SEQ ID NO:4)

Translation:
GSMMSKLGVLLTICLLLFPLTALPLDEDQPVHRPAERMQDISSDQHLFFDLIKRCCELPC GPGFCVPCC (SEQ ID NO:5)

Toxin Sequence:
Cys-Cys-Xaa1-Leu-Xaa3-Cys-Gly-Xaa3-Gly-Phe-Cys-Val-Xaa3-Cys-Cys-^ (SEQ ID NO:6)

Name: A3.1
Species: aurisiacus
Cloned: Yes

DNA Sequence:
CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG TTTGCTTCTGTTTCCCCTTACTGCTCTTCCGATGGATGGAGATCAATCTGTAGACCGA CCTGAAGAGCGTATGCAGGACGACATTTCATCTGAGCAGCATCCCTTGTTTAATCAG AAAAGAATGTGTTGCGGCGAAGGCCGGAAATGCCCCAGCTATTTCAGAAACAGTCA GATTTGTCATTGTTGTTAAATGACAACGTGTCGATGACCAACTTCGTTATCACGACT AATGAATAAGTAAAACGATTGCAGT (SEQ ID NO:7)

Translation:
MMSKLGVLLTICLLLFPLTALPMDGDQSVDRPEERMQDDISSEQHPLFNQKRMCCGEG RKCPSYFRNSQICHCC (SEQ ID NO:8)

Toxin Sequence:
Met-Cys-Cys-Gly-Xaa1-Gly-Arg-Lys-Cys-Xaa3-Ser-Xaa5-Phe-Arg-Asn-Ser-Gln-Ile-Cys-His-Cys-Cys-^ (SEQ ID NO:9)

Name: A3.2
Species: aurisiacus
Cloned: Yes

DNA Sequence:
GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTTTGCTTCTGTTTCCCC TTACTGCTCTTCCGATCGATGGAGATCAATCTGTAGACCGACCTGCAGAGCGTATGC AGGATGACATTTCATCTGAGCAGCATCGCTTGTTCAATCAGAAAAGAAGGTGCTGC CGGTGGCCATGCCCCCGACAAATCGACGGTGAATATTGTGGCTGTTGCCTTGGATGA TAACCGTGTTGATGACCAACTTTCTCGAG (SEQ ID NO:10)

Translation:
GSMMSKLGVLLTICLLLFPLTALPIDGDQSVDRPAERMQDDISSEQHRLFNQKRRCCRW PCPRQIDGEYCGCCLG (SEQ ID NO:11)

Toxin Sequence:
Cys-Cys-Arg-Xaa4-Xaa3-Cys-Xaa3-Arg-Gln-Ile-Asp-Gly-Xaa1-Xaa5-Cys-Gly-Cys-Cys-Leu-# (SEQ ID NO:12)

Name: A3.3
Species: aurisiacus
Cloned: Yes

DNA Sequence:
GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTACTTCTGTTTCCCC TTACTGCTTTTCCGATGGATGGAGATCAACCTGCAGACCAACCTGCAGATCGTATGC AGGACGACATTTCATCTGAGCAGTATCCCTTGTTTGATAAGAGACAAAAGTGTTGCA CTGGGAAGAAGGGGTCATGCTCCGGCAAAGCATGCAAAAATCTCAAATGTTGCTCT GGACGATAACGTGTTGATGACCAACTTTCTCGAG (SEQ ID NO:13)

Translation:
GSMMSKLGVLLTICLLLFPLTAFPMDGDQPADQPADRMQDDISSEQYPLFDKRQKCCT GKKGSCSGKACKNLKCCSGR (SEQ ID NO:14)

Toxin Sequence:
Xaa2-Lys-Cys-Cys-Thr-Gly-Lys-Lys-Gly-Ser-Cys-Ser-Gly-Lys-Ala-Cys-Lys-Asn-Leu-Lys-Cys-Cys-Ser-# (SEQ ID NO:15)

Name: A3.4
Species: aurisiacus
Cloned: Yes

DNA Sequence:
GGATCCATGATGTCTAAACTGGGAGTCTTGCTGACCATCTGTCTGCTTCTGTTTCCAC
TTACTGCTGTTCCGCTGGATGGAGATCAACCTCTAGACCGACACGCGGAGCGTATGC
ATGATGGCATTTCACCTAAACGCCATCCCTGGTTTGATCCCGTCAAACGGTGTTGCA
AGGTGCAATGCGAGTCTTGCACCCCTTGTTGCTAACGTGTTGATGACCAACTTTCTC
GAG (SEQ ID NO:16)

Translation:
GSMMSKLGVLLTICLLLFPLTAVPLDGDQPLDRHAERMHDGISPKRHPWFDPVKRCCK
VQCESCTPCC (SEQ ID NO:17)

Toxin Sequence:
Cys-Cys-Lys-Val-Gln-Cys-Xaa1-Ser-Cys-Thr-Xaa3-Cys-Cys-^ (SEQ ID NO:18)

Name: Bn3.1
Species: bandanus
Cloned: Yes

DNA Sequence:
GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTATGCTTCTGTTTCCCC
TCACTGCTCTTCCGATGGATGGAGATCAACCTGCAGACCGACCTGCAGAGCGTAGT
CAGGACGTTTCATCTGAACAGCATCCCTTGTTTGATCCCGTCAAACGGTGTTGCAAC
TGGCCATGCTCCATGGGATGCATCCCTTGTTGCTACTATTAATAACGTGTTGATGAC
CAACTTTCTCGAG (SEQ ID NO:19)

Translation:
GSMMSKLGVLLTICMLLFPLTALPMDGDQPADRPAERSQDVSSEQHPLFDPVKRCCNW
PCSMGCIPCCYY (SEQ ID NO:20)

Toxin Sequence:
Cys-Cys-Asn-Xaa4-Xaa3-Cys-Ser-Met-Gly-Cys-Ile-Xaa3-Cys-Cys-Xaa5-Xaa5-^ (SEQ ID NO:21)

Name: Bt3.1
Species: betulinus
Cloned: Yes

DNA Sequence:
CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCTTCTG

TCTGCTTCTGTTTCCCCTGACTGCTCTTCCGCTGGATGAAGATCAACCTGCAGACCG
ACCTGCAGAGCGTATGCAGGACATTTCATCTGAACAGCATCCCTTGTTTGATCCCGT
CAAACGGTGTTGCGAATTGCCATGCCATGGATGCGTCCCTTGTTGCTGGCCTTAATA
ACGTGTGGATGACCAACTGTGTTATCACGGCCACGTCAAGTGTCTAATGAATAAGT
AAAATGATTGCAGT (SEQ ID NO:22)

Translation:
MMSKLGVLLTFCLLLFPLTALPLDEDQPADRPAERMQDISSEQHPLFDPVKRCCELPCH
GCVPCCWP (SEQ ID NO:23)

Toxin Sequence:
Cys-Cys-Xaa1-Leu-Xaa3-Cys-His-Gly-Cys-Val-Xaa3-Cys-Cys-Xaa4-Xaa3-^ (SEQ ID NO:24)

Name: Bt3.2
Species: betulinus
Cloned: Yes

DNA Sequence:
CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCTTCTG
TCTGCTTCTGTTTCCCCTGACTGCTCTTCCGCTGGATGAAGATCAACCTGCAGACCG
ACATGCAGAGCGTATGCAGGACATTTCACCTGAACAGCATCCCTCGTTTGATCCCGT
CAAACGGTGTTGCGGGCTGCCATGCAATGGATGCGTCCCTTGTTGCTGGCCTTCATA
ACGTGTGGACGACCAACTTTGTTATCACGGCCACGTCAAGTGTCTGATGAATAAGTA
AAACGATTGCAGT (SEQ ID NO:25)

Translation:
MMSKLGVLLTFCLLLFPLTALPLDEDQPADRHAERMQDISPEQHPSFDPVKRCCGLPCN
GCVPCCWPS (SEQ ID NO:26)

Toxin Sequence:
Cys-Cys-Gly-Leu-Xaa3-Cys-Asn-Gly-Cys-Val-Xaa3-Cys-Cys-Xaa4-Xaa3-Ser-^ (SEQ ID NO:27)

Name: Bt3.3
Species: betulinus
Cloned: Yes

DNA Sequence:
CAAGAGGGATCGATAGCAGTTCATGATGTTTAAACTGGGAGTCTTGTTGACCATCTA
TATGCTTCTGTTTCCCTTTACTGCTCTTCCGCTGGATGGAGATCAACCTGCAGACCAA
CCTCTAGAGCGCATGCAGTATGACATGTTACGTGCAGTGAATCCCTGGTTTGATCCC
GTCAAAAGGTGCTGCTCGAGGAACTGCGCAGTATGCATCCCTTGTTGCCCGAATTGG
CCAGCTTGATTATCGCGGCCAAGAGTCTAATGAATAAGTAAAACGATTGCAGT (SEQ ID NO:28)

Translation:
MMFKLGVLLTIYMLLFPFTALPLDGDQPADQPLERMQYDMLRAVNPWFDPVKRCCSR NCAVCIPCCPNWPA (SEQ ID NO:29)

Toxin Sequence:
Cys-Cys-Ser-Arg-Asn-Cys-Ala-Val-Cys-Ile-Xaa3-Cys-Cys-Xaa3-Asn-Xaa4-Xaa3-Ala-^ (SEQ ID NO:30)

Name: Bu3.1
Species: bullatus
Cloned: Yes

DNA Sequence:
CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG TCTGCTTCTGTTTCCCCTTTTTGCTCTTCCGCAGGATGGAGATCAACCTGCAGACCGA CCTGCAGAGCGTATGCAGGACGACATTTCATCTGAGCAGAATTCCTTGCTTGAGAA GAGAGTTACTGACAGGTGCTGCAAAGGGAAGAGGGAATGCGGCAGATGGTGCAGA GATCACTCGCGTTGTTGCGGTCGACGATAAGCTGTTGATGACCAGCTTTGTTATCAC GGCTACATCAAGTGTCTAGTGAATAAGTAAAATGATTGCAGT (SEQ ID NO:31)

Translation:
MMSKLGVLLTICLLLFPLFALPQDGDQPADRPAERMQDDISSEQNSLLEKRVTDRCCKG KRECGRWCRDHSRCCGRR (SEQ ID NO:32)

Toxin Sequence:
Val-Thr-Asp-Arg-Cys-Cys-Lys-Gly-Lys-Arg-Xaa1-Cys-Gly-Arg-Xaa4-Cys-Arg-Asp-His-Ser-Arg-Cys-Cys-# (SEQ ID NO:33)

Name: Bu3.1A
Species: bullatus
Cloned: Yes

DNA Sequence:
CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG TCTGCTTCTGTTTCCCCTTTTTGCTCTTCGGCAGGATGGAGATCAACCTGCAGACCGA CCTGCAGAGCGTATGCAGGATGACATTTCATCTGAGCAGAATCCCTTGCTTGAGAA GAGAGTTGGTGACAGGTGCTGCAAAGGGAAGAGGGGGTGCGGCAGATGGTGCAGA GATCACTCACGTTGTTGCGGTCGACGATAACGTGTTGATGACCAGCTTTGTTATCAC GGCTACATCAAGTGTCTTAGTGATTAAGTAAAACGATTGCAGT (SEQ ID NO:34)

Translation:
MMSKLGVLLTICLLLFPLFALRQDGDQPADRPAERMQDDISSEQNPLLEKRVGDRCCK GKRGCGRWCRDHSRCCGRR (SEQ ID NO:35)

Toxin Sequence:
Val-Gly-Asp-Arg-Cys-Cys-Lys-Gly-Lys-Arg-Gly-Cys-Gly-Arg-Xaa4-Cys-Arg-Asp-His-Ser-Arg-Cys-Cys-# (SEQ ID NO:36)

Name: Bu3.2
Species: bullatus
Cloned: Yes

DNA Sequence:
CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG TCTGCTTCTGTTTCCCCTTTTTGCTCTTCCGCAGGATGGAGATCAACCTGCAGACCGA CCTGCAGAGCGTATGCAGGACGACATTTCATCTGAGCAGAATCCCTTGCTTGAGAA GAGAGTTGGTGAAAGGTGCTGCAAAAACGGGAAGAGGGGGTGCGGCAGATGGTGC AGAGATCACTCACGTTGTTGCGGTCGACGATAACGTGTTGATGACCGAGGCTTTCGT TATCACGGCTACATCAAGTGTCTAGTGAATAAGTAAAACGATTGCAGT (SEQ ID NO:37)

Translation:
MMSKLGVLLTICLLLFPLFALPQDGDQPADRPAERMQDDISSEQNPLLEKRVGERCCKN GKRGCGRWCRDHSRCCGRR (SEQ ID NO:38)

Toxin Sequence:
Val-Gly-Xaa1-Arg-Cys-Cys-Lys-Asn-Gly-Lys-Arg-Gly-Cys-Gly-Arg-Xaa4-Cys-Arg-Asp-His-Ser-Arg-Cys-Cys-# (SEQ ID NO:39)

Name: Bu3.3
Species: bullatus
Cloned: Yes

DNA Sequence:
CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG TCTGCTTCTGTTTCCCCTTTTTGCTCTTCCGCAGGACGGAGATCAACCTGCAGACCG ACCTGCAGAGCGTATGCAGGACGACCTTTCATCTGAGCAGCATCCCTTGTTTGAGAA GAGAATTGTTGACAGGTGCTGCAACAAAGGGAACGGGAAGAGGGGGTGCAGCAGA TGGTGCAGAGATCACTCACGTTGTTGCGGTCGACGATGAACTGTTGATGACCGAGG CTTTGGTTATCACGGCTACATCAAGTGTCTAGTGAATAAGTAAAACGATTGCAGT (SEQ ID NO:40)

Translation:
MMSKLGVLLTICLLLFPLFALPQDGDQPADRPAERMQDDLSSEQHPLFEKRIVDRCCNK GNGKRGCSRWCRDHSRCCGRR (SEQ ID NO:41)

Toxin Sequence:
Ile-Val-Asp-Arg-Cys-Cys-Asn-Lys-Gly-Asn-Gly-Lys-Arg-Gly-Cys-Ser-Arg-Xaa4-Cys-Arg-Asp-His-Ser-Arg-Cys-Cys-# (SEQ ID NO:42)

Name: Bu3.4
Species: bullatus
Cloned: Yes

DNA Sequence:
CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG TCTGCTTCTGTTTCCCCTTTTTGCTCTTCCGCAGGATGGAGATCAACCTGCAGACCGA CCTGCTGAGCGTATGCAGGACGACATTTCATCTGAGCGGAATCCCTTGTTTGAGAAG AGCGTTGGTTTATATTGCTGCCGACCCAAACCCAACGGGCAGATGATGTGCGACAG ATGGTGCGAAAAAAACTCACGTTGTTGCGGTCGACGATAATGTGTTGATGACCAGC TTTGTTATCAAGGCTACATCAAGTATCTAGTGAATAAGTAAAACGATTGCAGT (SEQ ID NO:43)

Translation:
MMSKLGVLLTICLLLFPLFALPQDGDQPADRPAERMQDDISSERNPLFEKSVGLYCCRP KPNGQMMCDRWCEKNSRCCGRR (SEQ ID NO:44)

Toxin Sequence:
Val-Gly-Leu-Xaa5-Cys-Cys-Arg-Xaa3-Lys-Xaa3-Asn-Gly-Gln-Met-Met-Cys-Asp-Arg-Xaa4-Cys-Xaa1-Lys-Asn-Ser-Arg-Cys-Cys-# (SEQ ID NO:45)

Name: Bu3.5
Species: bullatus
Cloned: Yes

DNA Sequence:
CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTTTTGTTGACCATCTG TCTGCTTCTGTTTCCCCTTACTGCTCTTCCGATGGATGGAGATCAATCTGTAGACCGA CCTGCAGAACGTATGCAGGACGACCTTTCATCTGAGCAGCATCCCTTGTTTGTTCAG AAAAGAAGGTGTTGCGGCGAAGGCTTGACATGCCCCAGATATTGGAAAAACAGTCA GATTTGTGCTTGTTGTTAAATGACAACGTGTCGATGACCAACTTCGGTATCACGACT ACGCCAAGTGTCTAATGAATAAGTAAAACGATTGCAGT (SEQ ID NO:46)

Translation:
MMSKLGVLLTICLLLFPLTALPMDGDQSVDRPAERMQDDLSSEQHPLFVQKRRCCGEG LTCPRYWKNSQICACC (SEQ ID NO:47)

Toxin Sequence:
Arg-Cys-Cys-Gly-Xaa1-Gly-Leu-Thr-Cys-Xaa3-Arg-Xaa5-Xaa4-Lys-Asn-Ser-Gln-Ile-Cys-Ala-Cys-Cys-^ (SEQ ID NO:48)

Name: Bu3.5A
Species: bullatus
Cloned: Yes

DNA Sequence:
CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG TCTGCTTCTGTTTCCCCTTTTTGCTCTTCCGCAGGATGGAGATCAACCTGCAGACCGA CCTGCTGAGCGTATGCAGGACGACATTTCATCTGAGCAGGATCCCTTGTTTGTTCAG AAAAGAAGGTGTTGCGGCGAAGGCTTGACATGCCCCAGATATTGGAAAAACAGTCA GATTTGTGCTTGTTGTTAAATGACAACGTGTGATGACCAACTTCGGTATCACGACTA CGCCAAGTGTCTAATGAATAAGTAAAACGATTGCAGT (SEQ ID NO:49)

Translation:
MMSKLGVLLTICLLLFPLFALPQDGDQPADRPAERMQDDISSEQDPLFVQKRRCCGEGL TCPRYWKNSQICACC (SEQ ID NO:50)

Toxin Sequence:
Arg-Cys-Cys-Gly-Xaa1-Gly-Leu-Thr-Cys-Xaa3-Arg-Xaa5-Xaa4-Lys-Asn-Ser-Gln-Ile-Cys-Ala-Cys-Cys-^ (SEQ ID NO:51)

Name: Cp3.1
Species: capitaneus
Cloned: Yes

DNA Sequence:
GGATCCATGATGTCTAAACTGGGAGTCTTGGTGACCATCTGCCTGCTTCTGTTTCCC CTTGCTGCTTTTCCACTGGATGGAAATCAACCTGCAGACCACCCTGCAAAGCGTACG CAAGATGACAGTTCAGCTGCCCTGATCAATACCTGGATTGATCATTCCCATTCTTGC TGCAGGGACTGCGGTGAAGATTGTGTTGGTTGTTGCCGGTAACGTGTTGATGACCAA CTTTCTCGAG (SEQ ID NO:52)

Translation:
GSMMSKLGVLVTICLLLFPLAAFPLDGNQPADHPAKRTQDDSSAALINTWIDHSHSCCR DCGEDCVGCCR (SEQ ID NO:53)

Toxin Sequence:
Ser-Cys-Cys-Arg-Asp-Cys-Gly-Xaa1-Asp-Cys-Val-Gly-Cys-Cys-Arg-^ (SEQ ID NO:54)

Name: Ca3.1
Species: caracteristicus
Cloned: Yes

DNA Sequence:
CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG TCTGCTTCTGTTTCCCCTTACTGCTCTTCCAATGGATGGAGATCAACCTGCAGACCA

ACCTGCAGATCGTATGCAGGACGACATTTCATCTGAGCAGTATCCCTTGTTTGATAT GAGAAAAAGGTGTTGCGGCCCCGGCGGTTCATGCCCCGTATATTTCAGAGACAATT TTATTTGTGGTTGTTGTTAAATGACAACGTGTCGATGACCAACTTCATTATCACGAC TACGCCAAGTGTCTAATGAATAAGTAAAATGATTGCAGT (SEQ ID NO:55)

Translation:
MMSKLGVLLTICLLLFPLTALPMDGDQPADQPADRMQDDISSEQYPLFDMRKRCCGPG GSCPVYFRDNFICGCC (SEQ ID NO:56)

Toxin Sequence:
Cys-Cys-Gly-Xaa3-Gly-Gly-Ser-Cys-Xaa3-Val-Xaa5-Phe-Arg-Asp-Asn-Phe-Ile-Cys-Gly-Cys-Cys-^ (SEQ ID NO:57)

Name: Ca3.2
Species: caracteristicus
Cloned: Yes

DNA Sequence:
CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG TCTGCTTCTGTTTCCCCTTACTGCTCTTCCGATGGATGGAGATGAACCTGCAAACCG ACCTGTCGAGCGTATGCAGGACAACATTTCATCTGAGCAGTATCCCTTGTTTGAGAA GAGACGAGATTGTTGCACTCCGCCGAAGAAATGCAAAGACCGACAATGCAAACCCC AGAGATGTTGCGCTGGACGATAACGTGTTGATGACCAACTTTATCACGGCTACGTCA AGTGTTTAGTGAATAAGTAAAATGATTGCAGT (SEQ ID NO:58)

Translation:
MMSKLGVLLTICLLLFPLTALPMDGDEPANRPVERMQDNISSEQYPLFEKRRDCCTPPK KCKDRQCKPQRCCAGR (SEQ ID NO:59)

Toxin Sequence:
Arg-Asp-Cys-Cys-Thr-Xaa3-Xaa3-Lys-Lys-Cys-Lys-Asp-Arg-Gln-Cys-Lys-Xaa3-Gln-Arg-Cys-Cys-Ala-# (SEQ ID NO:60)

Name: Ca3.3
Species: caracteristicus
Cloned: Yes

DNA Sequence:
CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG TCTGCTTCTGTTTCCCCTTACTGCTCTTCCACTGGATGGAGATCAACCTGCAGATCAA TCTGCAGAGCGACCTGCAGAGCGTACGCAGGACGACATTCAGCAGCATCCGTTATA TGATCCGAAAAGAAGGTGTTGCCGTTATCCATGCCCCGACAGCTGCCACGGATCTTG CTGCTATAAGTGATAACATGTTGATGGCCAGCTTTGTTATCACGGCCACGTCAAGTG TCTTAATGAATAAGTAAAACGATTGCAGT (SEQ ID NO:61)

Translation:
MMSKLGVLLTICLLLFPLTALPLDGDQPADQSAERPAERTQDDIQQHPLYDPKRRCCRYPCPDSCHGSCCYK (SEQ ID NO:62)

Toxin Sequence:
Arg-Cys-Cys-Arg-Xaa5-Xaa3-Cys-Xaa3-Asp-Ser-Cys-His-Gly-Ser-Cys-Cys-Xaa5-Lys-^ (SEQ ID NO:63)

Name: Ca3.4
Species: caracteristicus
Cloned: Yes

DNA Sequence:
CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGCCTTGTTGACCATCTGTCTACTTCTGTTTTCCCTTACTGCTGTTCCGCTGGATGGAGATCAACATGCAGACCAACCTGCACAGCGTCTGCAGGACCGCATTCCAACTGAAGATCATCCCTTATTTGATCCCAACAAACGGTGTTGCCCGCCGGTGGCATGCAACATGGGATGCAAGCCTTGTTGTGGATGACCAGCTTTGTTATCGCGGTCTTCATGAAGTGTCTTAATGAATAAGTAAAATGATTGCAGT (SEQ ID NO:64)

Translation:
MMSKLGALLTICLLLFSLTAVPLDGDQHADQPAQRLQDRIPTEDHPLFDPNKRCCPPVACNMGCKPCCG (SEQ ID NO:65)

Toxin Sequence:
Cys-Cys-Xaa3-Xaa3-Val-Ala-Cys-Asn-Met-Gly-Cys-Lys-Xaa3-Cys-Cys-# (SEQ ID NO:66)

Name: Ca3.5
Species: caracteristicus
Cloned: Yes

DNA Sequence:
CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGCCTTGTTGACCATCTGTCTACTTCTGTTTTCCCTAACTGCTGTTCCGCTGGATGGAGATCAACATGCAGACCAACCTGCAGAGCGTCTGCATGACCGCCTTCCAACTGAAAATCATCCCTTATATGATCCCGTCAAACGGTGTTGCGATGATTCGGAATGCGACTATTCTTGCTGGCCTTGCTGTATGTTTGGATAACCTTTGTTATCGCGGCCTCATCAAGTGTCTAATGAATAAGTAAAACGATTGCAGT (SEQ ID NO:67)

Translation:
MMSKLGALLTICLLLFSLTAVPLDGDQHADQPAERLHDRLPTENHPLYDPVKRCCDDSECDYSCWPCCMFG (SEQ ID NO:68)

Toxin Sequence:
Cys-Cys-Asp-Asp-Ser-Xaa1-Cys-Asp-Xaa5-Ser-Cys-Xaa4-Xaa3-Cys-Cys-Met-Phe-# (SEQ ID

NO:69)

Name: Ca3.6
Species: caracteristicus
Cloned: Yes

DNA Sequence:
GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCC
TTACTGCTGTTCCGCTGGATGGAGATCAACCTGCAGACCGACCTGCAGAGCGTAAG
CAGGACGTTTCATCTGAACAGCATCCCTTCTTTGATCCCGTCAAACGGTGTTGCCGC
CGGTGTTACATGGGATGCATCCCTTGTTGCTTTTAACGTGTTGATGACCAACTTTCTC
GAG (SEQ ID NO:70)

Translation:
GSMMSKLGVLLTICLLLFPLTAVPLDGDQPADRPAERKQDVSSEQHPFFDPVKRCCRRC
YMGCIPCCF (SEQ ID NO:71)

Toxin Sequence:
Cys-Cys-Arg-Arg-Cys-Xaa5-Met-Gly-Cys-Ile-Xaa3-Cys-Cys-Phe-^ (SEQ ID NO:72)

Name: Cr3.1
Species: circumcisus
Cloned: Yes

DNA Sequence:
CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGGGTATTGTTGACCATCT
GTCTGCTTCTGTTTCCCCTTACTGCTCTTCCAATGGATGGAGATCAACCTGCAGACC
AACCTGCAGATCGTATGCAGGACGACATTTCATCTGAGCAGTATCCCTTGTTTGATA
AGAGACGAAAGTGTTGCGGCAAAGACGGGCCATGCCCCAAATATTTCAAAGACAAT
TTTATTTGTGGTTGTTGTTAAATGACAACGTGTCGATGACCAACTTCGTTATCACGAT
TCGCCAAGTGTCTTAATGAATAAGTAAAATGATTGCAGT (SEQ ID NO:73)

Translation:
MMSKLGVLLTICLLLFPLTALPMDGDQPADQPADRMQDDISSEQYPLFDKRRKCCGKD
GPCPKYFKDNFICGCC (SEQ ID NO:74)

Toxin Sequence:
Arg-Lys-Cys-Cys-Gly-Lys-Asp-Gly-Xaa3-Cys-Xaa3-Lys-Xaa5-Phe-Lys-Asp-Asn-Phe-Ile-Cys-Gly-Cys-Cys-^ (SEQ ID NO:75)

Name: Da3.1
Species: dalli
Cloned: Yes

DNA Sequence:
CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGCCTTGTTGACCATCTGTCTACTTCTGTTTTCCCTAACTGCTGTTCCGCTGGATGGAGATCAACATGCAGACCAACCTGCAGAGCGTCTGCAGGACCGCCTTCCAACTGAAAATCATCCCTTATATGATCCCGTCAAACGGTGTTGCGATGATTCGGAATGCGACTATTCTTGCTGGCCTTGCTGTATTTTATCATAACCTTTGTTATCGCGGCCTCATCAAGTGTCAAATGAATAAGTAAAATGATTGCAGT (SEQ ID NO:76)

Translation:
MMSKLGALLTICLLLFSLTAVPLDGDQHADQPAERLQDRLPTENHPLYDPVKRCCDDSECDYSCWPCCILS (SEQ ID NO:77)

Toxin Sequence:
Cys-Cys-Asp-Asp-Ser-Xaa1-Cys-Asp-Xaa5-Ser-Cys-Xaa4-Xaa3-Cys-Cys-Ile-Leu-Ser-^ (SEQ ID NO:78)

Name: Da3.2
Species: dalli
Cloned: Yes

DNA Sequence:
CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATTTGTCTACTTCTGTTTCCCCTTACTGCTGTTCCACTGGATGGAGATCAGCCTGCAGACCGACCTGCAGAGCGTATGCAGGACGGCATTTCATCTGAACATCATCCATTTTTTGATTCCGTCAAAAAGAAACAACAGTGTTGCCCGCCGGTGGCATGCAACATGGGATGCGAGCCTTGTTGTGGATGACCAGCTTTGTTATCGCGGCTCATGAAGTGTCCTAATGAATAAGTAAAACGATTGCAGT (SEQ ID NO:79)

Translation:
MMSKLGVLLTICLLLFPLTAVPLDGDQPADRPAERMQDGISSEHHPFFDSVKKKQQCCPPVACNMGCEPCCG (SEQ ID NO:80)

Toxin Sequence:
Xaa2-Gln-Cys-Cys-Xaa3-Xaa3-Val-Ala-Cys-Asn-Met-Gly-Cys-Xaa1-Xaa3-Cys-Cys-# (SEQ ID NO:81)

Name: Da3.3
Species: dalli
Cloned: Yes

DNA Sequence:
CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGATCATATGTCTATTTCTGTTTCCCCTTACTGCTGTTCAGCTCAATGGAGATCAGCCTGCAGACCAATCTGCAGAGCGTATGCAGGACAAAATTTCATCTGAACATCATCCCTTTTTTGATCCCGTCAAACGTTGTTGCAACGCGGGGTTTTGCCGCTTCGGATGCACGCCTTGTTGTTGG

TGACCAGCTTTGTTATCGCGGCCTCATCAAGTGTCTAATGAATAAGTAAAATGATTG CAGT (SEQ ID NO:82)

Translation:
MMSKLGVLLIICLFLFPLTAVQLNGDQPADQSAERMQDKISSEHHPFFDPVKRCCNAGF CRFGCTPCCW (SEQ ID NO:83)

Toxin Sequence:
Cys-Cys-Asn-Ala-Gly-Phe-Cys-Arg-Phe-Gly-Cys-Thr-Xaa3-Cys-Cys-Xaa4-^ (SEQ ID NO:84)

Name: Di3.1
Species: distans
Cloned: Yes

DNA Sequence:
CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGCTGACCATCTT TCTGCTTCTGTTTCCCCTTACTGCTGTTCCGCTGGATGGAGATCAACCCGCAGACGG ACTTGCAGAGCGCATGCAGGACGACAGTTCAGCTGCACTGATTAGAGACTGGCTTC TTCAAACCCGACAGTGTTGTGTGCATCCATGCCCATGCACGCCTTGCTGTAGATGAC CAGCTTTGTCATCGCGGCTACGTCAAGTATCTAATGAATAAGTAAGTAAAACGATTG CAGT (SEQ ID NO:85)

Translation:
MMSKLGVLLTIFLLLFPLTAVPLDGDQPADGLAERMQDDSSAALIRDWLLQTRQCCVH PCPCTPCCR (SEQ ID NO:86)

Toxin Sequence:
Xaa2-Cys-Cys-Val-His-Xaa3-Cys-Xaa3-Cys-Thr-Xaa3-Cys-Cys-Arg-^ (SEQ ID NO:87)

Name: E3.1
Species: ermineus
Cloned: Yes

DNA Sequence:
ACCTCAAGAGGGATCGATCGCAGTTCATGATGTCTAAACTGGGAGCCTTGTTGACC ATCTGTCTGCTTCTGTTTCCCATTACTGCTCTTCTGATGGATGGAGATCAGCCTGCAG ACCGACCTGCAGAGCGTACGGAGGATGACATTTCATCTGACTACATTCCCTGTTGCA GTTGGCCATGCCCCCGATACTCCAACGGTAAACTTGTTTGTTTTTGTTGCCTTGGATG ATAATGTGTTGATGACCAACTTTGTTATCACGGCTACGTCAAGTGTCTACTGAATAA GTAAAATGATTGCAGTA (SEQ ID NO:88)

Translation:
MMSKLGALLTICLLLFPITALLMDGDQPADRPAERTEDDISSDYIPCCSWPCPRYSNGKL VCFCCLG (SEQ ID NO:89)

Toxin Sequence:
Cys-Cys-Ser-Xaa4-Xaa3-Cys-Xaa3-Arg-Xaa5-Ser-Asn-Gly-Lys-Leu-Val-Cys-Phe-Cys-Cys-Leu-# (SEQ ID NO:90)

Name: Ge3.2
Species: generalis
Cloned: Yes

DNA Sequence:
GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGGTTCTGTTTCCCC
TTACTGCTCTTCCACTGGATGGAGAACAACCTGTAGACCGACATGCCGAGCATATGC
AGGATGACAATTCAGCTGCACAGAACCCCTGGGTTATTGCCATCAGACAGTGTTGC
ACGTTCTGCAACTTTGGATGCCAACCTTGTTGCCTCACCTGATAACGTGTTGATGAC
CAACTTTCTCGAG (SEQ ID NO:91)

Translation:
GSMMSKLGVLLTICLVLFPLTALPLDGEQPVDRHAEHMQDDNSAAQNPWVIAIRQCCT
FCNFGCQPCCLT (SEQ ID NO:92)

Toxin Sequence:
Xaa2-Cys-Cys-Thr-Phe-Cys-Asn-Phe-Gly-Cys-Gln-Xaa3-Cys-Cys-Leu-Thr-^ (SEQ ID NO:93)

Name: Ge3.3
Species: generalis
Cloned: Yes

DNA Sequence:
GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGGTTCTGTTTCCCC
TTACTGCTCTTCCACTGGATGGAGAACAACCTGTAGACCGACATGCCGAGCATATGC
AGGATGACAATTCAGCTGCACAGAACCCCTGGGTTATTGCCATCAGACAGTGTTGC
ACGTTCTGCAACTTTGGATGCCAGCCTTGTTGCGTCCCCTGATAACGTGTTGATGAC
CAACTTTCTCGAG (SEQ ID NO:94)

Translation:
GSMMSKLGVLLTICLVLFPLTALPLDGEQPVDRHAEHMQDDNSAAQNPWVIAIRQCCT
FCNFGCQPCCVP (SEQ ID NO:95)

Toxin Sequence:
Xaa2-Cys-Cys-Thr-Phe-Cys-Asn-Phe-Gly-Cys-Gln-Xaa3-Cys-Cys-Val-Xaa3-^ (SEQ ID NO:96)

Name: μ-GIIIA
Species: geographus
Cloned: Yes

DNA Sequence:
GTCGACTCTAGAGGATCCGACAACAAAGAGTCAACCCCACTGCCACGTCAAGAGCG
AAGCGCCACAGCTAAGACAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGG
AGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCCTTACTGCTCTTCCGATGGATGGA
GATGAACCTGCAAACCGACCTGTCGAGCGTATGCAGGACAACATTTCATCTGAGCA
GTATCCCTTGTTTGAGAAGAGACGAGATTGTTGCACTCCGCCGAAGAAATGCAAAG
ACCGACAATGCAAACCCCAGAGATGTTGCGCTGGACGATAACGTGTTGATGACCAA
CTTTATCACGGCTACGTCAAGTGTTTAGTGAATAAGTAAAATGATTGCAGTCTTGCT
CAGATTTGCTTTTGTGTTTTGGTCTAAAGATCAATGACCAAACCGTTGTTTTGATGCG
GATTGTCATATATTTCTCGATTCCAATCCAACACTAGATGATTTAATCACGATAGAT
TAATTTTCTATCAATGCCTTGATTTTTCGTCTGTCATATCAGTTTTGTTTATATTTATT
TTTTCGTCACTGTCTACACAAACGCATGCATGCACGCATGCACGCACACACGCACGC
ACGCTCGCACAAACATGCGCGCGCACGCACACACACACACACACACACAAACACA
CACACAAGCAATCACACAATTATTGACATTATTTATTTATTCATTGATGTATTTGTTA
TTCGTTTGCTTGTTTTTAGAATAGTTTGAGGCCGTCTTTTTGGATTTATTTGAACTGC
TTTATTGTATACGAGTACTTCGTGCTTTGAAACACTGCTGAAAATAAAACAAACACT
GACGTAGC (SEQ ID NO:97)

Translation:
MMSKLGVLLTICLLLFPLTALPMDGDEPANRPVERMQDNISSEQYPLFEKRRDCCTPPK
KCKDRQCKPQRCCAGR (SEQ ID NO:98)

Toxin Sequence:
Arg-Asp-Cys-Cys-Thr-Xaa3-Xaa3-Lys-Lys-Cys-Lys-Asp-Arg-Gln-Cys-Lys-Xaa3-Gln-Arg-Cys-Cys-Ala-# (SEQ ID NO:99)

Name: μ-GIIIB
Species: geographus
Isolated: Yes
Cloned: Yes

DNA Sequence:
GGCCAGACGACAACAAAGAGTCAACCCCACTGCCACGTCAAGAGCGAAGCGCCAC
AGCTAAGACAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTT
GACCATCTGTCTGCTTCTGTTTCCCCTTACTGCTCTTCCGATGGATGGAGATGAACCT
GCAAACCGACCTGTCGAGCGTATGCAGGACAACATTTCATCTGAGCAGTATCCCTTG
TTTGAGAAGAGACGAGATTGTTGCACTCCGCCGAGGAAATGCAAAGACCGACGATG
CAAACCCATGAAATGTTGCGCTGGACGATAACGTGTTGATGACCAACTTTATCACG
GCTAGCTCAGTGTTTAGTGAATAAGTAAAATGATTGCAGTCTTGCTCAGATTGCTTT
TGTGTTTTGGTCTAAGATCAATGACCAAACCGTTGTTTTGATGCGGATTGTCATATA
TTTCTCGATTCCAATCCAACACTAGATGATTTAATCACGATAGATTAATTTTCTATCA
ATGCCTTGATTTTTCGTCTGTCATATCAGTTTTGTTTATATTTATTTTTTCGTCACTGT
CTACACAAACGCATGCATGCACGCATGCACGCACACACGCACGCACGCTCGCACAA
ACATGCGCGCGCACGCACACACACACACACACACACAAACACACACACGAAGCAATC
ACACAATTAGTTGACATTATTTATTTATTCATTGATGTATTTGTTATTCGTTTGCTTGT

TTTTAGAATAGTTTGAGGCCGTCTTTTTGGATTTATTTGAACTGCTTTATTGTATACG AGTACTTCGTGCTTTGAAACACTGCTGAAAATAAAACAAACACTGACGTAGCAAAA AAAAAAA (SEQ ID NO:100)

Translation:
MMSKLGVLLTICLLLFPLTALPMDGDEPANRPVERMQDNISSEQYPLFEKRRDCCTPPR KCKDRRCKPMKCCAGR (SEQ ID NO:101)

Toxin Sequence:
Arg-Asp-Cys-Cys-Thr-Xaa3-Xaa3-Arg-Lys-Cys-Lys-Asp-Arg-Arg-Cys-Lys-Xaa3-Met-Lys-Cys-Cys-Ala-# (SEQ ID NO:102)

Name: μ-GIIIC
Species: geographus
Isolated: Yes

Toxin Sequence:

Arg-Asp-Cys-Cys-Thr-Xaa3-Xaa3-Lys-Lys-Cys-Lys-Asp-Arg-Arg-Cys-Lys-Xaa3-Leu-Lys-Cys-Cys-Ala-# (SEQ ID NO:103)

Name: Gm3.1
Species: gloriamaris
Cloned: Yes

DNA Sequence:
CTCACTATAGGAATTCGAGCTCGGTACACGGGATCGATAGCAGTTCATGATGTCTAA ACTGGGAGCCTTGTTGACCATCTGTCTACTTCTGTTTTCCCTAACTGCTGTTCCGCTG GATGGAGATCAACATGCAGACCAACCTGCAGAGCGTCTGCATGACCGCCTTCCAAC TGAAAATCATCCCTTATATGATCCCGTCAAACGGTGTTGCGATGATTCGGAATGCGA CTATTCTTGCTGGCCTTGCTGTATGTTTGGATAACCTTTGTTATCGCGGCCTCGATAA GTGTCTAATGAATAAGTAAAACGATTGCAGTAGGC (SEQ ID NO:104)

Translation:
MMSKLGALLTICLLLFSLTAVPLDGDQHADQPAERLHDRLPTENHPLYDPVKRCCDDSE CDYSCWPCCMFG (SEQ ID NO:105)

Toxin Sequence:
Cys-Cys-Asp-Asp-Ser-Xaa1-Cys-Asp-Xaa5-Ser-Cys-Xaa4-Xaa3-Cys-Cys-Met-Phe-# (SEQ ID NO:106)

Name: Gm3.2
Species: gloriamaris
Cloned: Yes

DNA Sequence:
GTTCATGATGTCTAAACTGGGAGTCTTGTTGATCATCTGTCTACTTCTGTTTCCCCTT
ACTGCTGTTCCGCTGGATGGAGATCAACCTGCAGACCGATATGCAGAGCGTATGCA
GGACGACATTTCATCTGAACATCATCCCATGTTTGATGCCGTCAGAGGGTGTTGCCA
TCTGTTGGCATGCCGCTTCGGATGCTCGCCTTGTTGTTGGTGATCAGCTTTGTTATCG
CGGCCTCATCAAGTGACTCTAATGCAAA (SEQ ID NO:107)

Translation:
MMSKLGVLLIICLLLFPLTAVPLDGDQPADRYAERMQDDISSEHHPMFDAVRGCCHLLA
CRFGCSPCCW (SEQ ID NO:108)

Toxin Sequence:
Gly-Cys-Cys-His-Leu-Leu-Ala-Cys-Arg-Phe-Gly-Cys-Ser-Xaa3-Cys-Cys-Xaa4-^ (SEQ ID NO:109)

Name: Gm3.3
Species: gloriamaris
Cloned: Yes

DNA Sequence:
GAGACGACAAGGAACAGTCAACCCCACAGCCACGCCAAGAGCAGACAGCCACAGC
TACGTGAAGAAGGGTGGAGAGAGGTTCGTGATGTTGAAAATGGGAGTGGTGCTATT
CATCTTCCTGGTACTGTTTCCCCTGGCAACGCTCCAGCTGGATGCAGATCAACCTGT
AGAACGATATGCGGAGAACAAACAGCTCCTCAACCCAGATGAAAGGAGGGAAATC
ATATTGCATGCTCTGGGGACGCGATGCTGTTCTTGGGATGTGTGCGACCACCCGAGT
TGTACTTGCTGCGGCGGTTAGCGCCGAACATCCATGGCGCTGTGCTGGGCGGTTTTA
TCCAACAACGACAGCGTTTGTTGATTTCATGTATCATTGCGCCCACGTCTCTTGTCTA
AGAATGACGAACATGATTGCACTCTGGTTCAGATTTCGTGTTCTTTTCTGACAATAA
ATGACAAAACTCCAAAAAA (SEQ ID NO:110)

Translation:
MLKMGVVLFIFLVLFPLATLQLDADQPVERYAENKQLLNPDERREIILHALGTRCCSWD
VCDHPSCTCCGG (SEQ ID NO:111)

Toxin Sequence:
Cys-Cys-Ser-Xaa4-Asp-Val-Cys-Asp-His-Xaa3-Ser-Cys-Thr-Cys-Cys-Gly-# (SEQ ID NO:112)

Name: La3.1
Species: laterculatus
Cloned: Yes

DNA Sequence:
CGACCTCAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGA
CCATCTGTCTGCTTCTGTTTCCCCTTACTGCTCTTCCGATGGATGGAGATCAACCTGC

AGACCGACCTGCAGAGCGTATGCAGGACGTTTCATCTGAACAGCATCCCTTGTATG ATCCCGTCAAACGGTGTTGCGACTGGCCATGCAGCGGATGCATCCCTTGTTGCTAAT AGTAACAACGTGTTGATAACCAACTTTCTTACCACGACTACGTCAAGTGTCTAATGA ATAAGTAAAATGATTGCAGT (SEQ ID NO:113)

Translation:
MMSKLGVLLTICLLLFPLTALPMDGDQPADRPAERMQDVSSEQHPLYDPVKRCCDWPC SGCIPCC (SEQ ID NO:114)

Toxin Sequence:
Cys-Cys-Asp-Xaa4-Xaa3-Cys-Ser-Gly-Cys-Ile-Xaa3-Cys-Cys-^ (SEQ ID NO:115)

Name: La3.2
Species: laterculatus
Cloned: Yes

DNA Sequence:
CGACCTCAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGA CCATCTGTCTGCTTCTGTTTCCCCTTACTGCTCTGGATGGAGATCAACCTGCAGACC GACTTGCAGAGCGTATGCAGGACGACATTTCATCTGAGCAGCATCCCTTTGAAAAG AGACGAGACTGTTGCACACCTCCGAAGAAATGCAGAGACCGACAATGCAAACCTGC ACGTTGTTGCGGAGGATAACGTGTTGATGACCAACTTTGTTATCACGGCTACGTCAA GTGTCTAGTGAATAAGTAAAACGATTGCAGT (SEQ ID NO:116)

Translation:
MMSKLGVLLTICLLLFPLTALDGDQPADRLAERMQDDISSEQHPFEKRRDCCTPPKKCR DRQCKPARCCGG (SEQ ID NO:117)

Toxin Sequence:
Arg-Asp-Cys-Cys-Thr-Xaa3-Xaa3-Lys-Lys-Cys-Arg-Asp-Arg-Gln-Cys-Lys-Xaa3-Ala-Arg-Cys-Cys-Gly-# (SEQ ID NO:118)

Name: La3.3
Species: laterculatus
Cloned: Yes

DNA Sequence:
GGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGC TTCTGTTTCCCCTTACTGCTCTTCCGATGGATGGAGATCAACTTGCACGCCGATCTGC AGAGCGTATGCAGGACAACATTTCATCTGAGCAGCATCACCTCTTTGAAAAGAGAC GACCACCATGTTGCACCTATGACGGGAGTTGCCTAAAAGAATCATGCATGCGTAAA GCTTGTTGCGGATGATAACGTGTTGATGACCAACTTTGTTATCACGGCTACTCAAGT GTCTAATGAATAAGTAAAATGATTGCAGTA (SEQ ID NO:119)

Translation:

MMSKLGVLLTICLLLFPLTALPMDGDQLARRSAERMQDNISSEQHHLFEKRRPPCCTYD GSCLKESCMRKACCG (SEQ ID NO:120)

Toxin Sequence:
Arg-Xaa3-Xaa3-Cys-Cys-Thr-Xaa5-Asp-Gly-Ser-Cys-Leu-Lys-Xaa1-Ser-Cys-Met-Arg-Lys-Ala-Cys-Cys-# (SEQ ID NO:121)

Name: La3.3A
Species: laterculatus
Cloned: Yes

DNA Sequence:
GGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCACCTGTCTGC TTCTGTTTCCCCTTACTGCTCTTCCGATGGATGGAGATCAACTTGCACGCCGACCTG CAGAGCGTATGCAGGACAACATTTCATCTGAGCAGCATCCCTTCTTTGAAAGGAGA CGACCACCATGTTGCACCTATGACGGGAGTTGCCTAAAAGAATCATGCAAGCGTAA AGCTTGTTGCGGATAATAACGTGTTGATGACCAACTTTGTTATCACGGCTACTCAAG TGTCTAATGAATAAGTAAAATGATTGCAGTA (SEQ ID NO:122)

Translation:
MMSKLGVLLTTCLLLFPLTALPMDGDQLARRPAERMQDNISSEQHPFFERRRPPCCTYD GSCLKESCKRKACCG (SEQ ID NO:123)

Toxin Sequence:
Arg-Xaa3-Xaa3-Cys-Cys-Thr-Xaa5-Asp-Gly-Ser-Cys-Leu-Lys-Xaa1-Ser-Cys-Lys-Arg-Lys-Ala-Cys-Cys-# (SEQ ID NO:124)

Name: Lp3.1
Species: leopardus
Cloned: Yes

DNA Sequence:
GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCGTCTGTCTGCTTCTGTTTCCCC TTACTGCTCTTCGGCTGGTTGGAGATCAACCTGCAGAGCGACCTGCAAAGCGTACGC AGGACGACATTCCAGATGGACAGCATCCGTTAAATGATAGGCAGATAAACTGTTGC CCGTGGCCATGCCCTAGTACATGCCGCCATCAATGCTGCCATTAATGATAACGTGTT GATGACCAACTTTCTCGAG (SEQ ID NO:125)

Translation:
GSMMSKLGVLLTVCLLLFPLTALRLVGDQPAERPAKRTQDDIPDGQHPLNDRQINCCP WPCPSTCRHQCCH (SEQ ID NO:126)

Toxin Sequence:
Xaa2-Ile-Asn-Cys-Cys-Xaa3-Xaa4-Xaa3-Cys-Xaa3-Ser-Thr-Cys-Arg-His-Gln-Cys-Cys-His-^ (SEQ ID NO:127)

Name: Lv3.1
Species: lividus
Cloned: Yes

DNA Sequence:
GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCGTCTGTCTGCTTCTGTTTCCCC TTACTGCTCTTCGGCTGGTTAGAGATCAACCTGCAGAGCGACCTGCAAAGCGTACGC AGGACGACATTCCAAATGGACAGGATCCGTTAATTGATAGGCAGATAAATTGTTGC CCTTGGCCATGCCCTGATTCATGCCACTATCAATGCTGCCACTGATAACGTGTTGAT GACCAACTTTCTCGAG (SEQ ID NO:128)

Translation:
GSMMSKLGVLLTVCLLLFPLTALRLVRDQPAERPAKRTQDDIPNGQDPLIDRQINCCPW PCPDSCHYQCCH (SEQ ID NO:129)

Toxin Sequence:
Xaa2-Ile-Asn-Cys-Cys-Xaa3-Xaa4-Xaa3-Cys-Xaa3-Asp-Ser-Cys-His-Xaa5-Gln-Cys-Cys-His-^ (SEQ ID NO:130)

Name: L3.1
Species: lynceus
Cloned: Yes

DNA Sequence:
AAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTG CTTCTGTTTCCCCTTACTGCTCTTCCGATGGATGGAGATCAATCTGCAGACCGACTTG CAGAGCGTATGCAGGACAACATTTCATCTGAGCAGCATCCCTTCTTTGAAAAGAGA GGACGAGACTGTTGCACACCTCCGAGGAAATGCAGAGACCGAGCCTGCAAACCTCA ACGTTGTTGCGGAGGATAAGCTGTTGATGACCAACTTTGTTATACGGC (SEQ ID NO:131)

Translation:
MMSKLGVLLTICLLLFPLTALPMDGDQSADRLAERMQDNISSEQHPFFEKRGRDCCTPP RKCRDRACKPQRCCGG (SEQ ID NO:132)

Toxin Sequence:
Gly-Arg-Asp-Cys-Cys-Thr-Xaa3-Xaa3-Arg-Lys-Cys-Arg-Asp-Arg-Ala-Cys-Lys-Xaa3-Gln-Arg-Cys-Cys-Gly-# (SEQ ID NO:133)

Name: M3.1
Species: magus
Cloned: Yes

DNA Sequence:
CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG
TCTGCTTCTGTTTCCCCTTACTGCTCTTCCGATGGATGGAGATGAACCTGCAAACCG
ACCTGTCGAGCGTATGCAGGACAACATTTCATCTGAGCAGTATCCCTTGTTTGAGAA
GAGACGAGATTGTTGCACTCCGCCGAAGAAATGCAAAGACCGACAATGCAAACCCC
AGAGATGTTGCGCTGGACGATAACGTGTTGATGACCAACTTTATCACGGCTACGTCA
AGTGTTTAGTGAATAAGTAAAATGATTGCAGTCTTGCTCAGATTTGCTTTTGTGTTTT
GGTCTAAAGATCAATGACCAAACCGTTGTTTTGATGCGGATTGTCATATATTTCTCG
ATTCCAATCCAACACTAGATGATTTAATCACGATAGATTAATTTTCTATCAATGCCT
TGATTTTTCGTCTGTCATATCAGTTTTGTTTATATTTATTTTTTCGTCACTGTCTACAC
AAACGCATGCATGCACGCATGCACGCACACACGCACGCACGCTCGCACAAACATGC
GCGCGCACGCACACACACACACACACACACAAACACACACACGAAGCAATCACAC
AATTAGTTGACATTATTTATTTATTCATTGATGTATTTGTTATTCGTTTGCTTGTTTTT
AGAATAGTTTGAGGCCGTCTTTTTGGATTTATTTGAACTGCTTTATTGTATACGAGTA
CTTCGTGCGGGGAAACACTGCTGAAAATAAAACAAACACTGACGTAGCAAAAAAA
AAAAA (SEQ ID NO:134)

Translation:
MMSKLGVLLTICLLLFPLTALPMDGDEPANRPVERMQDNISSEQYPLFEKRRDCCTPPK
KCKDRQCKPQRCCAGR (SEQ ID NO:135)

Toxin Sequence:
Arg-Asp-Cys-Cys-Thr-Xaa3-Xaa3-Lys-Lys-Cys-Lys-Asp-Arg-Gln-Cys-Lys-Xaa3-Gln-Arg-Cys-Cys-Ala-# (SEQ ID NO:136)

Name: M3.2
Species: magus
Cloned: Yes

DNA Sequence:
CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG
TCTGCTTCTGTTTCCCCTTACTGCTCTTCCAATGGATGGAGATCAACCTGCAGACCA
ACCTGCAGATCGTATGCAGGACGACATTTCATCTGAGCAGTATCCCTTGTTTGATAT
GAGAAAAAGGTGTTGCGGCCCCGGCGGTTCATGCCCCGTATATTTCAGAGACAATT
TTATTTGTGGTTGTTGTTAAATGACAACGTGTCGATGACCAACTTCATTATCACGAC
TACGCCAAGTGTCTAATGAATAAATAAAATGATTGCAGTCTCGCTCAGATTTGCTTT
TGTATTTTGGTCTAAAGATCAATGACCAAACCGTTGTTTTGGTGTGGATTTTCATATA
TTTCTCGAGTCCTATCCAACACTAGATGATTTAATCACGATAGATCTGATTTTTTTAT
CAAAGGCTTGGTTTTTCGTCTGTCACATCAGTTTTGTTTATATTTAATTTTTCGTCACT
GATTACACACACGCATGAACGCACAGAGTACTAACACATACACACACACACACACA
CACACACACACACACACACACACACACACACACACACACACGCGCGCGCGCGGCG
CCATCTAGTAGCGCCGCGACGACACACAC (SEQ ID NO:137)

Translation:
MMSKLGVLLTICLLLFPLTALPMDGDQPADQPADRMQDDISSEQYPLFDMRKRCCGPG
GSCPVYFRDNFICGCC (SEQ ID NO:138)

Toxin Sequence:
Cys-Cys-Gly-Xaa3-Gly-Gly-Ser-Cys-Xaa3-Val-Xaa5-Phe-Arg-Asp-Asn-Phe-Ile-Cys-Gly-Cys-Cys-^ (SEQ ID NO:139)

Name: M3.3
Species: magus
Cloned: Yes

DNA Sequence:
CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG
TTTGCTTCTGTTTCCCCTTACTGCTCTTCCGAGGGATGGAGATCAATCTGTAGACCGA
CCTGCAGAGCGTATGCAGGACGACATTTCATCTGAGCTGCATCCCTTGTCAATCAGA
AAAAGAATGTGTTGCGGCGAGAGTGCGCCATGCCCCAGCTATTTCAGAAACAGTCA
GATTTGTCATTGTTGTTAAATGACAACGTGTCGATGACCACCTTCGTTATCACGACT
AATGATAAGTAAAATGATTGCAGTCTCGCTCAGATTTGCTTTTGTATTTTGGTCTAA
AGATCAATGACCAAACCGTTGTTTTGATGTGGATTTTCATATATTTCTCGAGTCCTAT
CCAACACTAGATGATTTAATCACGATAGATCTGATTTTTTTATCAAAGCCTTGGTTTT
TCGTCTGTCACATCAGTTTTGTTTATATTTAATTTTTCGTCACTGATTACACACACGC
ATGAACGCACAGACGTACTAACACATACACACACACACACACACACACACACACACAC
ACACACACACACACACACACAC (SEQ ID NO:140)

Translation:
MMSKLGVLLTICLLLFPLTALPRDGDQSVDRPAERMQDDISSELHPLSIRKRMCCGESAP
CPSYFRNSQICHCC (SEQ ID NO:141)

Toxin Sequence:
Met-Cys-Cys-Gly-Xaa1-Ser-Ala-Xaa3-Cys-Xaa3-Ser-Xaa5-Phe-Arg-Asn-Ser-Gln-Ile-Cys-His-Cys-Cys-^ (SEQ ID NO:142)

Name: M3.4
Species: magus
Cloned: Yes

DNA Sequence:
CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG
TCTGCTTCTGTTTCCCCTTACTGCTCTTCCAATGGATGGAGATCAACCTGCAGACCA
ACCTGCAGATCGTATGCAGGACGACATTTCATCTGAGCAGTATCCCTTGTTTGATAA
GAGACAAAAGTGTTGCGGCCCCGGCGGTTCATGCCCCGTATATTTCACAGACAATTT
TATTTGTGGTTGTTGTTAAATGACAACGTGTCGATGACCAACTTCATTATCACGACT
ACGCCAAGTGTCTAATGAATAAATAAAATGATTGCAGTCTCGCTCAGATTTGCTTTT
GTATTTGGTCTAAAGATCAATGACCAAACCGTTGTTTTGGTGCTGGATTTTCATATA
TTTCTCGATTCCTATCCAACACTAGATGATTTAATCACGATAGATCTGATTTTTTTAT
CAATGCCTTAATTTTTTGCTCTGTCATATCAGTTTTGTTTATAT (SEQ ID NO:143)

Translation:
MMSKLGVLLTICLLLFPLTALPMDGDQPADQPADRMQDDISSEQYPLFDKRQKCCGPG GSCPVYFTDNFICGCC (SEQ ID NO:144)

Toxin Sequence:
Xaa2-Lys-Cys-Cys-Gly-Xaa3-Gly-Gly-Ser-Cys-Xaa3-Val-Xaa5-Phe-Thr-Asp-Asn-Phe-Ile-Cys-Gly-Cys-Cys-^ (SEQ ID NO:145)

Name: M3.5
Species: magus
Cloned: Yes

DNA Sequence:
CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG TCTGCTTCTGTTTCCCCTTACTGCTCTTCCAATGGATGGAGATCAACCTGCAGACCA ACCTGCAGATCGTATGCAGGACGACATTTCATCTGAGCAGTATCCCTTGTTTGATAA GAGACAAAAGTGTTGCGGCCCCGGCGGTTCATGCCCCGTATATTTCAGAGACAATTT TATTTGTGGTTGTTGTTAAATGACAACGTGTCGATGACCATCTTCATTATCACGACT ACGCCAAGTGTCTAATGAATAAATAAAATGATTGCAGTCTCGCTCAGATTTGCTTTT GTATTTTGGTCTAAAGATCAATGACCAAACCGTTGTTTTGGTGTGGATTTTCATATAT TTCTCGATTCCTATCCAACACTAGATGATTTAATCACGATAGATCTGATTTTTT (SEQ ID NO:146)

Translation:
MMSKLGVLLTICLLLFPLTALPMDGDQPADQPADRMQDDISSEQYPLFDKRQKCCGPG GSCPVYFRDNFICGCC (SEQ ID NO:147)

Toxin Sequence:
Xaa2-Lys-Cys-Cys-Gly-Xaa3-Gly-Gly-Ser-Cys-Xaa3-Val-Xaa5-Phe-Arg-Asp-Asn-Phe-Ile-Cys-Gly-Cys-Cys-^ (SEQ ID NO:148)

Name: U001
Species: magus
Isolated: No

Toxin Sequence:
Xaa2-Lys-Cys-Cys-Ser-Gly-Gly-Ser-Cys-Xaa3-Leu-Xaa5-Phe-Arg-Asp-Arg-Leu-Ile-Cys-Xaa3-Cys-Cys-^ (SEQ ID NO:149)

Name: Comatose/Death
Species: marmoreus
Isolated: Yes

Toxin Sequence:

Ser-Lys-Gln-Cys-Cys-His-Leu-Ala-Ala-Cys-Arg-Phe-Gly-Cys-Thr-Xaa3-Cys-Cys-Asn-^ (SEQ ID NO:150)

Name: Mr3.1
Species: marmoreus
Cloned: Yes

DNA Sequence:
CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG
TCTGCTTCTGTTTCCCGTTACTGCTCTTCCGATGGATGGTGATCAACCTGCAGACCGA
CTTGTAGAGCGTATGCAGGACAACATTTCATCTGAGCAGCATCCCTTCTTTGAAAAG
AGAAGAGGAGGCTGTTGCACACCTCCGAGGAAATGCAAAGACCGAGCCTGCAAAC
CTGCACGTTGCTGCGGCCCAGGATAACGTGTTGATGACCAACTTTGTTATCACGGCT
ACGTCAAGTGTCTAGTGAATAAGTAAAACGATTGCAG (SEQ ID NO:151)

Translation:
MMSKLGVLLTICLLLFPVTALPMDGDQPADRLVERMQDNISSEQHPFFEKRRGGCCTPP
RKCKDRACKPARCCGPG (SEQ ID NO:152)

Toxin Sequence:
Arg-Gly-Gly-Cys-Cys-Thr-Xaa3-Xaa3-Arg-Lys-Cys-Lys-Asp-Arg-Ala-Cys-Lys-Xaa3-Ala-Arg-Cys-Cys-Gly-Xaa3-# (SEQ ID NO:153)

Name: Mr3.2
Species: marmoreus
Cloned: Yes

DNA Sequence:
GAGCTCGGTACCCCGACCTCAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTG
GGAATCTTGTTGACCATCTGTCTACTTCTATTTCCCCTTACTGCTGTTCCGCTGGATG
GAGATCAACCTGCAGACCGACCTGCAGAGCGTATGCAGGACGACATTTCATCTGAA
CATCATCCCTTTTTTGATCCCGTCAAACGGTGTTGCAGGTTATCATGCGGCCTGGGA
TGCCACCCTTGTTGTGGATGACCAGCTTTGTTATCGCGGCCTCATCAAGTGTCTAAT
GAATAAGTAAAA (SEQ ID NO:154)

Translation:
MMSKLGILLTICLLLFPLTAVPLDGDQPADRPAERMQDDISSEHHPFFDPVKRCCRLSCG
LGCHPCCG (SEQ ID NO:155)

Toxin Sequence:
Cys-Cys-Arg-Leu-Ser-Cys-Gly-Leu-Gly-Cys-His-Xaa3-Cys-Cys-# (SEQ ID NO:156)

Name: Mr3.3
Species: marmoreus

Cloned: Yes

DNA Sequence:
GGCCTACACCAAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCCCGATCGATAGCAGTTCATGATGTCTAGACTGGGAGTCTTGTTGACCATCTGTCTACTTCTGTTTCCCCTTACTGCTGTTCCGCTGGATGGAGATCAACCTGCGGACCGACCTGCAGAGCGCCTGCAGGACGACATTTCATCTGAACATCATCCCCATTTTGATTCCGGCAGAGAGTGTTGCGGTTCGTTCGCATGCCGCTTTGGATGCGTGCCTTGTTGTGTATGACCAGCTTTGTTATCACGGCCTCATCGAGTGTCTAATGAATAAGTAAAACGATTGCAGTAGGCGGGTACCGAGCTCGAATTCC (SEQ ID NO:157)

Translation:
MMSRLGVLLTICLLLFPLTAVPLDGDQPADRPAERLQDDISSEHHPHFDSGRECCGSFACRFGCVPCCV (SEQ ID NO:158)

Toxin Sequence:
Xaa1-Cys-Cys-Gly-Ser-Phe-Ala-Cys-Arg-Phe-Gly-Cys-Val-Xaa3-Cys-Cys-Val-^ (SEQ ID NO:159)

Name: Mr3.4
Species: marmoreus
Cloned: Yes

DNA Sequence:
CGACCTCAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTACTTCTATTTCCCCTTACTGCTGTTCCGCTGGATGGAGACCAACCTGCAGACCGACCTGCAGAGCGTATGCAGGACGACATTTCATCTGAACGTCATCCTTTTTTTGATCGCAGCAAACAGTGTTGCCATCTGCCGGCATGCCGCTTCGGATGTACGCCTTGTTGTTGGTGATCAGCTTTGTTATCGCGTCCTCATCAAGTGTCTAATGAATAAGTAAAATGATTGCAG (SEQ ID NO:160)

Translation:
MMSKLGVLLTICLLLFPLTAVPLDGDQPADRPAERMQDDISSERHPFFDRSKQCCHLPACRFGCTPCCW (SEQ ID NO:161)

Toxin Sequence:
Ser-Lys-Gln-Cys-Cys-His-Leu-Xaa3-Ala-Cys-Arg-Phe-Gly-Cys-Thr-Xaa3-Cys-Cys-Xaa4-^ (SEQ ID NO:162)

Name: Mr3.5
Species: marmoreus
Cloned: Yes

DNA Sequence:
GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCC

TTACTGCTCTTCCGCTGGATGGAGATCAACCTGCAGACCAACGTGCAGAGCGTACG
CAGGCCGAGAAGCATTCCTTGCCTGATCCGAGAATGGGCTGTTGCCCGTTTCCATGC
AAAACCAGTTGCACTACTTTGTGTTGCGGGTGATGATAACGTGTTGATGACCAACTT
TCTCGAG (SEQ ID NO:163)

Translation:
GSMMSKLGVLLTICLLLFPLTALPLDGDQPADQRAERTQAEKHSLPDPRMGCCPFPCKT
SCTTLCCG (SEQ ID NO:164)

Toxin Sequence:
Met-Gly-Cys-Cys-Xaa3-Phe-Xaa3-Cys-Lys-Thr-Ser-Cys-Thr-Thr-Leu-Cys-Cys-# (SEQ ID NO:165)

Name: U014
Species: marmoreus
Isolated: Yes

Toxin Sequence:
Cys-Cys-His-Xaa4-Asn-Xaa4-Cys-Asp-His-Leu-Cys-Ser-Cys-Cys-Gly-Ser-^ (SEQ ID NO:166)

Name: U017
Species: marmoreus
Cloned: Yes

DNA Sequence:
GCCAAGCTTGCATGCCTGCAGGATGACTCTAGAGGATCCCCACCTCAAGAGGGATC
GATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTACTTCTGTT
TGCCCTTACTGCTGTTCCGCTGGATGGAGATCAACCTGCAGACCGACCTGCAGAACG
TATGCAGGACGACATTTCATCTGAACGTCATCCCATGTTTGATGCCGTCAGAGATTG
TTGCCCGTTGCCGGCATGCCCCTTTGGATGCAACCCTTGTTGTGGATGACCAGCTTT
GTTATCGGGACCTCATCAAGTGTCTAATGAATAAGTAAAAAACGATTCGAGTGGGT
ACCGAGCTCGAATTCC (SEQ ID NO:167)

Translation:
MMSKLGVLLTICLLLFALTAVPLDGDQPADRPAERMQDDISSERHPMFDAVRDCCPLP
ACPFGCNPCCG (SEQ ID NO:168)

Toxin Sequence:
Asp-Cys-Cys-Xaa3-Leu-Xaa3-Ala-Cys-Xaa3-Phe-Gly-Cys-Asn-Xaa3-Cys-Cys-# (SEQ ID NO:169)

Name: U019
Species: marmoreus
Isolated: Yes

Toxin Sequence:
Cys-Cys-Ala-Xaa3-Ser-Ala-Cys-Arg-Leu-Gly-Cys-Arg-Xaa3-Cys-Cys-Arg-^ (SEQ ID NO:170)

Name: U020
Species: marmoreus
Isolated: Yes

Toxin Sequence:
Cys-Cys-Ala-Xaa3-Ser-Ala-Cys-Arg-Leu-Gly-Cys-Arg-Xaa3-Cys-Cys-Arg-^ (SEQ ID NO:171)

Name: U022
Species: marmoreus
Isolated: Yes

Toxin Sequence:
Cys-Cys-Ala-Xaa3-Ser-Ala-Cys-Arg-Leu-Gly-Cys-Arg-Xaa3-Cys-Cys-Arg-^ (SEQ ID NO:172)

Name: U024
Species: marmoreus
Isolated: Yes

Toxin Sequence:
Gly-Cys-Cys-Gly-Ser-Phe-Ala-Cys-Arg-Phe-Gly-Cys-Val-Xaa3-Cys-Cys-Val-^ (SEQ ID NO:173)

Name: Nb3.1
Species: nobilis
Cloned: Yes

DNA Sequence:
GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTACTTCTGTTTCCCC
TTACTGCTCTTCCGCTGGATGAAGATCAACCGGTACACCGACCTGCAGAGCGTATGC
AGGACATTTCATCTGATCAACATCTCTTCTTTGATCTCATCAAACGGTGCTGCGAGT
TGCCATGCGGGCCAGGCTTTTGCGTCCCTTGTTGCTGACATCAATAACGTGTTGATG
ACCAACTTTCTCGAG (SEQ ID NO:174)

Translation:
GSMMSKLGVLLTICLLLFPLTALPLDEDQPVHRPAERMQDISSDQHLFFDLIKRCCELPC
GPGFCVPCC (SEQ ID NO:175)

Toxin Sequence:
Cys-Cys-Xaa1-Leu-Xaa3-Cys-Gly-Xaa3-Gly-Phe-Cys-Val-Xaa3-Cys-Cys-^ (SEQ ID NO:176)

Name: Nb3.2
Species: nobilis
Cloned: Yes

DNA Sequence:
GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTACTTCTGTTTCCCC TTACTGCTTTTCCGATGGATGGAGATCAACCTGCAGACCAACCTGCAGATCGTATGC AGGACGACATTTCATCTGAGCAGTATCCCTTGTTTGATAAGAGACAAAAGTGTTGCA CTGGGAAGAAGGGGTCATGCTCCGGCAAAGCATGCAAAAATCTCAAATGTTGCTCT GGACGATAACGTGTTGATGACCAACTTTCTCGAG (SEQ ID NO:177)

Translation:
GSMMSKLGVLLTICLLLFPLTAFPMDGDQPADQPADRMQDDISSEQYPLFDKRQKCCT GKKGSCSGKACKNLKCCSGR (SEQ ID NO:178)

Toxin Sequence:
Xaa2-Lys-Cys-Cys-Thr-Gly-Lys-Lys-Gly-Ser-Cys-Ser-Gly-Lys-Ala-Cys-Lys-Asn-Leu-Lys-Cys-Cys-Ser-# (SEQ ID NO:179)

Name: Pu3.1
Species: pulicarius
Cloned: Yes

DNA Sequence:
GGATCCATGATGTCTAAACTGGGAGTTTTGTTGACCATCTGTCTGCTTCTGTTTCCCC TTACTGCTGTTCCGCTGGATGGAGATCAACCTGCAGACCGACCTGCAGAGCGTATGC AGGACATTGCAACTGAACAGCATCCCTTCTTTGATCCCGTCAAACGGTGTTGCAACA GCTGTTACATGGGATGCATCCCTTGTTGCTTCTAGTAATAACGTGTTGATGACCAAC TTTCTCGAG (SEQ ID NO:180)

Translation:
GSMMSKLGVLLTICLLLFPLTAVPLDGDQPADRPAERMQDIATEQHPFFDPVKRCCNSC YMGCIPCCF (SEQ ID NO:181)

Toxin Sequence:
Cys-Cys-Asn-Ser-Cys-Xaa5-Met-Gly-Cys-Ile-Xaa3-Cys-Cys-Phe-^ (SEQ ID NO:182)

Name: Qc3.1
Species: quercinus
Cloned: Yes

DNA Sequence:
GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCC

TTACAGCTCTTCAGCTGGATGGAGATCAACCTGCAGACCGACCTGCAGAGCGTACG
CAGGACATTGCATCTGAACAGTATCGAAAGTTTGATCAGAGACAGAGGTGTTGCCA
GTGGCCATGCCCCGGTAGTTGCAGATGCTGCCGTACTGGTTAACGTGTTGATGACCA
ACTTTCTCGAG (SEQ ID NO:183)

Translation:
GSMMSKLGVLLTICLLLFPLTALQLDGDQPADRPAERTQDIASEQYRKFDQRQRCCQW
PCPGSCRCCRTG (SEQ ID NO:184)

Toxin Sequence:
Xaa2-Arg-Cys-Cys-Gln-Xaa4-Xaa3-Cys-Xaa3-Gly-Ser-Cys-Arg-Cys-Cys-Arg-Thr-# (SEQ ID NO:185)

Name: QcIIIA
Species: quercinus
Isolated: Yes

Toxin Sequence:
Cys-Cys-Ser-Gln-Asp-Cys-Leu-Val-Cys-Ile-Xaa3-Cys-Cys-Xaa3-Asn-# (SEQ ID NO:186)

Name: QcIIIB
Species: quercinus
Isolated: Yes

Toxin Sequence:
Cys-Cys-Ser-Arg-His-Cys-Xaa4-Val-Cys-Ile-Xaa3-Cys-Cys-Xaa3-Asn-? (SEQ ID NO:187)

Name: R3.1
Species: radiatus
Isolated: Yes
Cloned: Yes

DNA Sequence:
TCAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCT
GTCTGCTTCTGTTTCCCCTTACTGCTCTTCCGATGGATGGAGATCAACCTGTAGACCG
ACTTGCAGAGCGTATGCAGGACAACATTTCATCTGAGCAGCATACCTTCTTTGAAAA
GAGACTACCATCGTGTTGCTCCCTTAACTTGCGGCTTTGCCCAGTACCAGCATGCAA
ACGTAACCCTTGTTGCACAGGATAACGTGTTGATGACCAACTTTGTTATCACGGCTA
CGTCAAGTGTCTAGTGAATAAGTAAAACGATTGCAGT (SEQ ID NO:188)

Translation:
MMSKLGVLLTICLLLFPLTALPMDGDQPVDRLAERMQDNISSEQHTFFEKRLPSCCSLN
LRLCPVPACKRNPCCTG (SEQ ID NO:189)

Toxin Sequence:
Leu-Xaa3-Ser-Cys-Cys-Ser-Leu-Asn-Leu-Arg-Leu-Cys-Xaa3-Val-Xaa3-Ala-Cys-Lys-Arg-Asn-Xaa3-Cys-Cys-Thr-# (SEQ ID NO:190)

Name: R3.2
Species: radiatus
Cloned: Yes

DNA Sequence:
AGGTCGACTCTAGAGGATCCCCAAGGATCGATAGCAGTTCATGATGTCTAAACTGG
GAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCCTTACTGCTCTTCCGATGGATGG
AGATCAACCTGCAGACCGACTTGCAGAGCGTATGCAGGACGACATTTCATCTGAGC
AGCATCCCTTCTTTAAAAAGAGACAACAAAGATGTTGCACCGTTAAGAGGATTTGT
CCAGTACCAGCATGCAGAAGTAAACCTTGTTGCAAATCATAACGTATTGATGACCA
ACTTTGTTATCACGGCTACGTCAAGTGTCTAGTGAATAAGTAAAATGATTGCAG
(SEQ ID NO:191)

Translation:
MMSKLGVLLTICLLLFPLTALPMDGDQPADRLAERMQDDISSEQHPFFKKRQQRCCTV
KRICPVPACRSKPCCKS (SEQ ID NO:192)

Toxin Sequence:
Xaa2-Gln-Arg-Cys-Cys-Thr-Val-Lys-Arg-Ile-Cys-Xaa3-Val-Xaa3-Ala-Cys-Arg-Ser-Lys-Xaa3-Cys-Cys-Lys-Ser-^ (SEQ ID NO:193)

Name: R3.3
Species: radiatus
Cloned: Yes

DNA Sequence:
ACCTCAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACC
ATCTGTCTGCTTCTGTTTCCCGTTACTGCTCTTCCGATGGATGGTGATCAACCTGCAG
ACCGACTTGTAGAGCGTATGCAGGACAACATTTCATCTGAGCAGCATCCCTTCTTTG
AAAAGAGAAGAGGAGGCTGTTGCACACCTCCGAGGAAATGCAAAGACCGAGCCTG
CAAACCTGCACGTTGCTGCGGCCCAGGATAACGTGTTGATGACCAACTTTGTTATCA
CGGCTACGTCAAGTGTCTAGTGAATAAGTAAAACGATTGCAGT (SEQ ID NO:194)

Translation:
MMSKLGVLLTICLLLFPVTALPMDGDQPADRLVERMQDNISSEQHPFFEKRRGGCCTPP
RKCKDRACKPARCCGPG (SEQ ID NO:195)

Toxin Sequence:
Arg-Gly-Gly-Cys-Cys-Thr-Xaa3-Xaa3-Arg-Lys-Cys-Lys-Asp-Arg-Ala-Cys-Lys-Xaa3-Ala-Arg-Cys-Cys-Gly-Xaa3-# (SEQ ID NO:196)

Name: Ra3.1
Species: rattus
Cloned: Yes

DNA Sequence:
GGATCCATGATGTCTAAACTGGGAGTCTTGGTGACCATCTGCCTGCTTCTGTTCCCT CTTGCTGCTTTTCCACTGGATGGAGATCAACCTGCAGACCACCCTGCAAAGCGTACG CAAGATGACAGTTCAGCTGCCCTGATCAATGCCTGGCTTGATGAATCCCAGACTTGC TGCAGTAACTGCGGTGAAGATTGTGATGGTTGTTGCCAGTAACGTGTTGATGACCAA CTTTCTCGAG (SEQ ID NO:197)

Translation:
GSMMSKLGVLVTICLLLFPLAAFPLDGDQPADHPAKRTQDDSSAALINAWLDESQTCCS NCGEDCDGCCQ (SEQ ID NO:198)

Toxin Sequence:
Xaa2-Thr-Cys-Cys-Ser-Asn-Cys-Gly-Xaa1-Asp-Cys-Asp-Gly-Cys-Cys-Gln-^ (SEQ ID NO:199)

Name: Sm3.1
Species: stercusmuscarum
Cloned: Yes

DNA Sequence:
GACCTCAAGAGGGATCGATAGCAGTTCGTGATGTCTAAACTGGGAGTCTTGTTGAC CATCTGTCTGCTTCTGTTTCCTCTTACTGCTCTTCCGATGGATGGAGATCAACCTGCA GACCAACCTGCAGATCGTATGCAGGACGACATTTCATCTGAGCAGTATCCCTTGTTT GATAAGAGACAAAAGTGTTGCACTGGGAAGAAGGGGTCATGCTCCGGCAAAGCAT GCAAAAATCTCAAATGTTGCTCTGGACGATAACGTGTTGATGACCAACTTTGTTATC ACGGCTACGTCAAGTGTCTAATGAATAAGTAAAACGATTGCAGT (SEQ ID NO:200)

Translation:
MSKLGVLLTICLLLFPLTALPMDGDQPADQPADRMQDDISSEQYPLFDKRQKCCTGKK GSCSGKACKNLKCCSGR (SEQ ID NO:201)

Toxin Sequence:
Xaa2-Lys-Cys-Cys-Thr-Gly-Lys-Lys-Gly-Ser-Cys-Ser-Gly-Lys-Ala-Cys-Lys-Asn-Leu-Lys-Cys-Cys-Ser-# (SEQ ID NO:202)

Name: U034
Species: stercusmuscarum
Isolated: Yes
Cloned: Yes

DNA Sequence:
GATCGATAGCAGTTCGTGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTT
CTGTTTCCCCTTACTGCTCTTCCGATGGATGGAGATCAACCTGCAGACCAACCTGCA
GATCGTATGCAGAACGACATTTCATCTGAGCAGTATCCCTTGTTTGATAAGAGACAA
AAGTGTTGCGGCCCCGGCGCGTCATGCCCCAGATATTTCAAAGACAATTTTATTTGT
GGTTGTTGTTAAATGACAACGTGTCGATGACCAACTTCGTTATCACGACTTCGCCAA
GTGTCTAATGAATAAGTAAAACGATTGCAGT (SEQ ID NO:203)

Translation:
MSKLGVLLTICLLLFPLTALPMDGDQPADQPADRMQNDISSEQYPLFDKRQKCCGPGAS
CPRYFKDNFICGCC (SEQ ID NO:204)

Toxin Sequence:
Xaa2-Lys-Cys-Cys-Gly-Xaa3-Gly-Ala-Ser-Cys-Xaa3-Arg-Xaa5-Phe-Lys-Asp-Asn-Phe-Ile-Cys-Gly-Cys-Cys-^ (SEQ ID NO:205)

Name: S3.1
Species: striatus
Cloned: Yes

DNA Sequence:
CGACCTTTCAAGAGGGATCGATAGCAGTTCGCGATGTCTAAACTGGGGGTATTGTTG
ACCATCTGTCTGCTTCTGTTTCCCCTTACTGCTCTTCCGATGGATGAAGATCAACCTG
CAGACCAACTTGAAGATCGTATGCAGGACGACATTTCATCTGAGCAGTATCCCTCGT
TTGTTAGGAGACAAAAGTGTTGCGGCGAAGGCTCGTCATGCCCCAAATATTTCAAA
AACAATTTTATTTGTGGTTGTTGTTAAATGACAACGTGTCGATGACCAACTTCGTTA
TCACGACTACGCCAAGTGTCTTGTCTAATGATAATAAAATGATTCC (SEQ ID NO:206)

Translation:
MSKLGVLLTICLLLFPLTALPMDEDQPADQLEDRMQDDISSEQYPSFVRRQKCCGEGSS
CPKYFKNNFICGCC (SEQ ID NO:207)

Toxin Sequence:
Xaa2-Lys-Cys-Cys-Gly-Xaa1-Gly-Ser-Ser-Cys-Xaa3-Lys-Xaa5-Phe-Lys-Asn-Asn-Phe-Ile-Cys-Gly-Cys-Cys-^ (SEQ ID NO:208)

Name: S3.2
Species: striatus
Cloned: Yes

DNA Sequence:
GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCGTCTGTCTGCTTCTGTTTCCCC
TTACTGCTCTTCCGCTGGATGGAGATCAACCTGCAGACCGACCTGCAGAGCGTATGC
AGGACGACATTTCATCTGACGAGCATCCCTTGTTTGATAAGAGACAAAACTGTTGCA

ATGGGGGATGCTCCAGCAAATGGTGCAGAGATCACGCACGTTGTTGCGGTCGATGA TAACGTGTTGATGACCAACTTTCTCGAG (SEQ ID NO:209)

Translation:
GSMMSKLGVLLTVCLLLFPLTALPLDGDQPADRPAERMQDDISSDEHPLFDKRQNCCN GGCSSKWCRDHARCCGR (SEQ ID NO:210)

Toxin Sequence:
Xaa2-Asn-Cys-Cys-Asn-Gly-Gly-Cys-Ser-Ser-Lys-Xaa4-Cys-Arg-Asp-His-Ala-Arg-Cys-Cys-# (SEQ ID NO:211)

Name: Ts3.1
Species: tessulatus
Cloned: Yes

DNA Sequence:
GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATGTGTCTGCTTCTGTTTCCCC TTACTGCTGTTCCGCTGGATGGAGATCAACCTGCAGACCGACCTGCAGAGCGTAGG CAGGACATTGCAACTGACGATCATCCTTTGTTTGATCCCGTCAAACGGTGCTGCCAC AAATGCTATATGGGATGCATCCCTTGTTGCATTTAGTAACGTGTTGATGACCAACTT TCTCGAG (SEQ ID NO:212)

Translation:
GSMMSKLGVLLTMCLLLFPLTAVPLDGDQPADRPAERRQDIATDDHPLFDPVKRCCHK CYMGCIPCCI (SEQ ID NO:213)

Toxin Sequence:
Cys-Cys-His-Lys-Cys-Xaa5-Met-Gly-Cys-Ile-Xaa3-Cys-Cys-Ile-^ (SEQ ID NO:214)

Name: Ts3.2
Species: tessulatus
Cloned: Yes

DNA Sequence:
GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTGTGCTTCTGTTTCCCC TTACTGCTGTTCCGCTGGATGGAGATCAACCTGCAGACCAACCTGCAGAGCGTACG CAGAACGAGCAGCATCCCTTGTATGATCAGAAAAGAAAGTGTTGCCGGCCGCCATG CGCCATGAGCTGCGGCATGGCTAGGTGTTGCTATTAATGATAACGTGTTGATGACCA ACTTTCTCGAG (SEQ ID NO:215)

Translation:
GSMMSKLGVLLTICVLLFPLTAVPLDGDQPADQPAERTQNEQHPLYDQKRKCCRPPCA MSCGMARCCY (SEQ ID NO:216)

Toxin Sequence:

Lys-Cys-Cys-Arg-Xaa3-Xaa3-Cys-Ala-Met-Ser-Cys-Gly-Met-Ala-Arg-Cys-Cys-Xaa5-^ (SEQ ID NO:217)

Name: Circling
Species: textile
Isolated: Yes
Cloned: Yes

DNA Sequence:
GAGTCAACCCACTGTCACGCCAAGAGCGGACGCCACAGCTAAGGCAAGAAGGATC
GATAGCAGTTCATGATGTCTAAACTGGGAGCCTTGTTGACCATCTGTCTACTTCTGT
TTTCCCTTACTGCTGTTCCGCTGGATGGAGATCAACATGCAGACCAACCTGCACAGC
GTCTGCAGGACCGCATTCCAACTGAAGATCATCCCTTATTTGATCCCAACAAACGGT
GTTGCCCGCCGGTGGCATGCAACATGGGATGCAAGCCTTGTTGTGGATGACCAGCTT
TGTTATCGCGGTCTCATGAAGTGTCTAATGAATAAGTAAAACGATTGCAGTTTCGTT
CAGATTTGCTGTTGTATTTTGGTCTAAAGATTAATGACCAAACTGTTCTTTTGATCCG
GATTTTCACGTATTTCTCGATTCCTATTCAACACTAGATAAGTTAATCACGACAGAT
CTGATTTTCCATCAATGCCTTGCTTTTTGGTCTGTCATATAAATCTTGTTTATATTTAA
TTTCTCGTCACTTTCAACACGCACACACACACACACACACACGCGCGCGC (SEQ ID NO:218)

Translation:
MMSKLGALLTICLLLFSLTAVPLDGDQHADQPAQRLQDRIPTEDHPLFDPNKRCCPPVA
CNMGCKPCCG (SEQ ID NO:219)

Toxin Sequence:
Cys-Cys-Xaa3-Xaa3-Val-Ala-Cys-Asn-Met-Gly-Cys-Lys-Xaa3-Cys-Cys-Gly-^ (SEQ ID NO:220)

Name: Scratcher I
Species: textile
Cloned: Yes

DNA Sequence:
GGATCCAGACGACAAAGAAGAGTCAACCCACTGCCACGTCAAGAGCAGAGCCCAC
AGCTAAGACAAGAAGGATCGATAGCAGTTCATGATGTTTAAACTGGGAGTCTTGTT
GACCATCTGTCTCCTTCTGTTTTCCCTTAATGCTGTTCCGTTGGATGGAGATCAACCT
GCAGACCAACCTGCAGAGCGTCTGCTGGACGACATTTCATTTGAAAATAATCCCTTT
TATGATCCCGCCAAACGGTGTTGCAGGACTTGCTTCGGTTGCACACCTTGTTGTGGA
TGACCAGCCTCATCAAGTGTCTAACGAATAAGTAAAGCGATTGCAGTCTCGTTCAG
ATTTACTTTTGTATTCTGGTCTAAAGATTAATGACCAAACTCTTCTTTTGATCCGGAT
GTACATATATTTCTCGATTCCTATCCAACGCTAGATAAGCTAATCACGACAGATCTG
ATTTTCTGTCAATGCCTTGCTTTTTGGTCTCTCATATCACTCTTGTTTATATTTAATTT
CTCGTCACTATATATATATATACACACACACACACACGGAATTCCGATTGTCCAGTA
CCGTTCTTGGGATCGAGGTATTGCTGCGATGGCTTATTCTGTACTCTTTTCTTCTGCG

CTTGATAGTGATGTCTTCTACTCCCATCTGTGCTACCCCTGGCTTGATCTTTGATAGG
CGTGTGCCCTTCACTGGTTATAAACCCCTCTGATCCTACTCTCTGGACGCCTCGGGG
GCCCAACCTCCAAATAAAGCGACATCCAATGAAAAAA (SEQ ID NO:221)

Translation:
MMFKLGVLLTICLLLFSLNAVPLDGDQPADQPAERLLDDISFENNPFYDPAKRCCRTCF
GCTPCCG (SEQ ID NO:222)

Toxin Sequence:
Cys-Cys-Arg-Thr-Cys-Phe-Gly-Cys-Thr-Xaa3-Cys-Cys-# (SEQ ID NO:223)

Name: Tx3.1
Species: textile
Cloned: Yes

DNA Sequence:
GGAACAGTCAACCCCACAGCCACGCCAAGAGCAGACAGCCACAGCTACGTGAAGA
AGGGTGGAGAGAGGTTCATGATGTTGAAAATGGGAGTGGTGCTATTCATCTTTCTGG
TACTGTTTCCCCTGGCAACGCTCCAGCTGGATGCAGATCAACCTGTAGAACGATATG
CGGAGAACAAACAGCTCCTCAACCCAGATGAAAGGAGGGAAATCCTATTGCCTGCT
CTGAGGAAGTTCTGCTGTGATTCGAATTGGTGCCACATTTCGGATTGTGAGTGCTGC
TACGGTTAGCGCCGAACATCCATGGCACTGTGCTGGGCGGTTTCATCCCAACAACG
ACAGCGTTTGTTGATTTCATGTATCATTGCGCCCACGTCTCTTGTCTAAGAATGACG
AACATGATTGCACTCTGGTTCAGATTTCGTGTTCTTTTCTGACAATAAATGACAAAcC
TCC (SEQ ID NO:224)

Translation:
MMLKMGVVLFIFLVLFPLATLQLDADQPVERYAENKQLLNPDERREILLPALRKFCCDS
NWCHISDCECCYG (SEQ ID NO:225)

Toxin Sequence:
Phe-Cys-Cys-Asp-Ser-Asn-Xaa4-Cys-His-Ile-Ser-Asp-Cys-Xaa1-Cys-Cys-Xaa5-# (SEQ ID NO:226)

Name: U031
Species: textile
Isolated: Yes
Cloned: Yes

DNA Sequence:
CAAGGAACAGTCAACCCCACAGCCACGCCAAGAGCAGACAGCCACAGCTACGTGA
AGAAGGGTGGAGAGAGGTTCGTGATGTTGAAAATGGGAGTGGTGCTATTCATCTTC
CTGGTACTGTTTCCCCTGGCAACGCTCCAGCTGGATGCAGATCAACCTGTAGAACGA
TATGCGGAGAACAAACAGCTCCTCAGCCCAGATGAAAGGAGGGAAATCATATTGCA
TGCTCTGGGGACGCGATGCTGTTCTTGGGATGTGTGCGACCACCCGAGTTGTACTTG

CTGCGGTTAGCGCCGAACATCCATGGCGCTGTGCTGGGCGGTTTTATCCCAACAACG ACAGCGTTTGTTGATTTCATGTATCATTGCGCCCACGTCTCTTGTCTAAGAATGACG AACATGATTGCACTCTGGTTCAGATTTCGTGTTCTTTTCTGACAATAAATGACAAAA CNCC (SEQ ID NO:227)

Translation:
MLKMGVVLFIFLVLFPLATLQLDADQPVERYAENKQLLSPDERREIILHALGTRCCSWD VCDHPSCTCCG (SEQ ID NO:228)

Toxin Sequence:
Cys-Cys-Ser-Xaa4-Asp-Val-Cys-Asp-His-Xaa3-Ser-Cys-Thr-Cys-Cys-# (SEQ ID NO:229)

Name: U032
Species: textile
Isolated: Yes
Cloned: Yes

DNA Sequence:
GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCC TTACTGCTCTTCCGCTGGATGGAGATCAACCCGCAGACCAAGCTGCAGAGCGTATG CAGGCCGAGCAGCATCCCTTGTTTGATCAGAAAAGACGGTGCTGCAAGTTTCCATG CCCCGATAGTTGCAGATATTTGTGTTGCGGGTGATGATAACGTGTTGATGACCAACT TTCTCGAG (SEQ ID NO:230)

Translation:
GSMMSKLGVLLTICLLLFPLTALPLDGDQPADQAAERMQAEQHPLFDQKRRCCKFPCP DSCRYLCCG (SEQ ID NO:231)

Toxin Sequence:
Arg-Cys-Cys-Lys-Phe-Xaa3-Cys-Xaa3-Asp-Ser-Cys-Arg-Xaa5-Leu-Cys-Cys-# (SEQ ID NO:232)

Name: T3.1
Species: tulipa
Cloned: Yes

DNA Sequence:
CGACCTCAAGAGGGATCGATAGCAGTTCATGTCTAAACTGGGAGTCTTGTTGACAA TCTGTCTGCTTCTGTTTCCCCTTACTGCTCTGCCGATGGATGGAGATGAACCTGCAG ACCGACCTGCAGAGCGTATGCAGGACAACATTTCATCTGAGCAGCATCCCTTGTTTG AGGAGAGACACGGATGTTGCAAGGGGCCCGAAGGATGCTCCTCCAGAGAATGCAG ACCCCAACATTGTTGCGGTCGACGATAACGTGTTGAGGGCCAACTTTGTTATCACGG CTACGTCAAGTGTTTAGTGAATAAGTAAAATGATTGCAG (SEQ ID NO:233)

Translation:

MSKLGVLLTICLLLFPLTALPMDGDEPADRPAERMQDNISSEQHPLFEERHGCCKGPEG CSSRECRPQHCCGRR (SEQ ID NO:234)

Toxin Sequence:
His-Gly-Cys-Cys-Lys-Gly-Xaa3-Xaa1-Gly-Cys-Ser-Ser-Arg-Xaa1-Cys-Arg-Xaa3-Gln-His-Cys-Cys-# (SEQ ID NO:235)

Name: Fi3.1
Species: figulinus
Cloned: Yes

DNA Sequence:
CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGCTGACCATCT GTCTGCTTCTGATTCCCCTTACTGCTCTTTCGCTGGATGGAGATCAACCTGCAGACC GACCTGCAGAGCGTATGCAGGATGGAATTTCATCTGAACAGCATCCCATGTTTGATC CCGTCAGACGGTGTTGCCCGTGGCCATGCAACATAGGATGCGTACCTTGTTGTTGAT GACCAGTTTTGTTATCGCGGCCTCATCAAATGTCTAATGAATAAGTAAAACGATTGC AGT (SEQ ID NO:236)

Translation:
MMSKLGVLLTICLLLIPLTALSLDGDQPADRPAERMQDGISSEQHPMFDPVRRCCPWPC NIGCVPCC (SEQ ID NO:237)

Toxin Sequence:
Cys-Cys-Xaa3-Xaa4-Xaa3-Cys-Asn-Ile-Gly-Cys-Val-Xaa3-Cys-Cys-^ (SEQ ID NO:238)

Name: Fi3.2
Species: figulinus
Cloned: Yes

DNA Sequence:
CAAGAGGGATCGATAGCAGTTCATGATGTTTAAACTGGGAGTCCTGTTGACCATCTG TATGCTTCTGTTTCCCTTTACTGCTCTTCCGCTGGATGGAGAGCAACCTGCAGACCA ACCTGCAGAGCGCATGCAGTATGACATGTTACGTGCAATGAATCCCTGGTTTGATCC CGTCAAAAGGTGCTGCTCGAAGAACTGCGCAGTATGCATCCCTTGTTGCCCGTAACT GACCAGCTTGATTATCGCGGCCAAGGCTCTAATGAATAAGTAAAACGATTGCAGT (SEQ ID NO:239)

Translation:
MMFKLGVLLTICMLLFPFTALPLDGEQPADQPAERMQYDMLRAMNPWFDPVKRCCSK NCAVCIPCCP (SEQ ID NO:240)

Toxin Sequence:
Cys-Cys-Ser-Lys-Asn-Cys-Ala-Val-Cys-Ile-Xaa3-Cys-Cys-Xaa3-^ (SEQ ID NO:241)

Name: Fi3.3
Species: figulinus
Cloned: Yes

DNA Sequence:
CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGAGAGTCTTGTTGACCTTATG TCTGCTTCTGTTTCCCCTTACTGCTCTTCCGCTGAATGAAGATCAACCTGCAGAGCGT ATGCAGGACGACAATTCATCTGAGCAGCACCCCTTGTATGACCACAAACGAAAGTG TTGCCGGTGGCCATGCCCCGCAAGATGCGGCTCTTGTTGCCTGTAATAACGTGTTGG CCAACTTTGTTATCACGGCCACGTCAAATGTTTAATGAATAAGTAAAACGATTGCAG T (SEQ ID NO:242)

Translation:
MMSKLRVLLTLCLLLFPLTALPLNEDQPAERMQDDNSSEQHPLYDHKRKCCRWPCPAR CGSCCL (SEQ ID NO:243)

Toxin Sequence:
Cys-Cys-Arg-Xaa4-Xaa3-Cys-Xaa3-Ala-Arg-Cys-Gly-Ser-Cys-Cys-Leu-^ (SEQ ID NO:244)

Name: Fi3.4
Species: figulinus
Cloned: Yes

DNA Sequence:
CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCTTATG TCTGCTTCTGTTTCCCCTGACTGCTCTTCCGCTGGATGAAGATCAAGCTGCAGACCG ACCTGCAGAGCGTATGCAGGGCATGTCATCTGAACAGCATCCCTTCTTTGATCCCGT CAAACGGTGTTGCGAGTTGTCACGCTGCCTTGGATGCGTCCCTTGTTGCACATCTTA ATAACGTGTGGATGACCAACTGTGTTATCACGGCCACGTCAAGTGTCTAATGAATA AGTAAAATGATTGCAGT (SEQ ID NO:245)

Translation:
MMSKLGVLLTLCLLLFPLTALPLDEDQAADRPAERMQGMSSEQHPFFDPVKRCCELSR CLGCVPCCTS (SEQ ID NO:246)

Toxin Sequence:
Cys-Cys-Xaa1-Leu-Ser-Arg-Cys-Leu-Gly-Cys-Val-Xaa3-Cys-Cys-Thr-Ser-^ (SEQ ID NO:247)

Name: Fi3.5
Species: figulinus
Cloned: Yes

DNA Sequence:

CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCTTATG TCTGCTTCTGTTTCCCCTGACTGCTCTTCCGCTGGATGAAGATCAACCTGCAGACCG ACCTGCAGAGCGTATGCAGGGCATGTCATCTGAACAGCATCCCTTCTTTGATCCCGT CAAACGGTGTTGCGAGTTGTCAAAATGCCATGGATGCGTCCCTTGTTGCATACCTTA ATAACGTGCGGATGACCAACTGTGTTATCACGGCCACGTCAAGTGTCTAATGAATA AGTAAAATGATTGCAGT (SEQ ID NO:248)

Translation:
MMSKLGVLLTLCLLLFPLTALPLDEDQPADRPAERMQGMSSEQHPFFDPVKRCCELSK CHGCVPCCIP (SEQ ID NO:249)

Toxin Sequence:
Cys-Cys-Xaa1-Leu-Ser-Lys-Cys-His-Gly-Cys-Val-Xaa3-Cys-Cys-Ile-Xaa3-^ (SEQ ID NO:250)

Name: Qc3.2
Species: quercinus
Cloned: Yes

DNA Sequence:
CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTCGGAGTCTTGTTGACCATCTG TCTGGTTCTGTTTCCCCTTACAGCTCTTCAGCTGGATGGAGATCAACCTGCAGACCG ACCTGCAGAGCGTACGCAGGACATTTCATCTGAACAGTATCGAAAGTTTGATCAGA GACAGAGGTGTTGCCGGTGGCCATGCCCCGGTAGTTGCAGATGCTGCCGTTATCGTT AACGTGTTGGTGACCAGCTTTGTTATCACGACCACGCCAAGTGTCTAACGAATAAGT AAAATGATTGCAGT (SEQ ID NO:251)

Translation:
MMSKLGVLLTICLVLFPLTALQLDGDQPADRPAERTQDISSEQYRKFDQRQRCCRWPCP GSCRCCRYR (SEQ ID NO:252)

Toxin Sequence:
Xaa2-Arg-Cys-Cys-Arg-Xaa4-Xaa3-Cys-Xaa3-Gly-Ser-Cys-Arg-Cys-Cys-Arg-Xaa5-Arg-^ (SEQ ID NO:253)

Name: Qc3.3
Species: quercinus
Cloned: Yes

DNA Sequence:
CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG TCTGCTTCTGTTTCCCCTTACTGCTCTTCCACTGGATGGAGATCAACCTGCAGATCAA TCTGCAGAGCGACCTGCAGAGCGTACGCAGGACGACATTCAGCAGCATCCGTTATA TGATCCGAAAAGAAGGTGTTGCCGTTATCCATGCCCCGACAGCTGCCACGGATCTTG CTGCTATAAGTGATAACATGTTGATGGCCAGCTTTGTTATCACGGCCACGTCAAGTG TCTAATGAATAAGTAAAACGATTGCAGT (SEQ ID NO:254)

Translation:
MMSKLGVLLTICLLLFPLTALPLDGDQPADQSAERPAERTQDDIQQHPLYDPKRRCCRY PCPDSCHGSCCYK (SEQ ID NO:255)

Toxin Sequence:
Arg-Cys-Cys-Arg-Xaa5-Xaa3-Cys-Xaa3-Asp-Ser-Cys-His-Gly-Ser-Cys-Cys-Xaa5-Lys-^ (SEQ ID NO:256)

Name: Wi3.1
Species: wittigi
Cloned: Yes

DNA Sequence:
GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCA TTACTGCTCTTCCGGTGGGTGGAGATCAGCCTGCAGACCGACTTGCAGAGCGTATGC AGGACGACACTTCATCTGAGCAGCATCCCTTTGAAAAGAGACTACCATCATGTTGC GACTTTGAGAGGCTTTGCGTAGTACCAGCATGCATACGTCATCAGTGTTGCACAGGA TAACGTGTTGATGACCAACTTTCTCGAG (SEQ ID NO:257)

Translation:
MMSKLGVLLTICLLLFPITALPVGGDQPADRLAERMQDDTSSEQHPFEKRLPSCCDFERL CVVPACIRHQCCTG (SEQ ID NO:258)

Toxin Sequence:
Leu-Xaa3-Ser-Cys-Cys-Asp-Phe-Xaa1-Arg-Leu-Cys-Val-Val-Xaa3-Ala-Cys-Ile-Arg-His-Gln-Cys-Cys-Thr-# (SEQ ID NO:259)

Name: bt3a
Species: betulinus
Isolated: Yes

Toxin Sequence:

Cys-Cys-Lys-Gln-Ser-Cys-Thr-Thr-Cys-Met-Xaa3-Cys-Cys-Xaa4-^ (SEQ ID NO:260)

Name: T3.2
Species: tulipa
Cloned: Yes

DNA Sequence:
GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACAATCTGTCTGCTTCTGTTTCCCC TTACTGCTCTGCCGATGGATGGAGATGAACCTGCAGACCGACCTGCAGAGCGTATG CAGGACAACATTTCATCTGAGCAGCATCCCTTGTTTGAGGAGAGACACGGATGTTG

CGAGGGGCCGAAGGGATGCTCCTCCAGAGAATGCAGACCCCAACATTGTTGCGGTC GACGATAACGTGTTGATGACCAACTNTCTCGAG (SEQ ID NO:261)

Translation:
MMSKLGVLLTICLLLFPLTALPMDGDEPADRPAERMQDNISSEQHPLFEERHGCCEGPK GCSSRECRPQHCCGRR (SEQ ID NO:262)

Toxin Sequence:
His-Gly-Cys-Cys-Xaa1-Gly-Xaa3-Lys-Gly-Cys-Ser-Ser-Arg-Xaa1-Cys-Arg-Xaa3-Gln-His-Cys-Cys-# (SEQ ID NO:263)

Name: A3.5
Species: aurisiacus
Cloned: Yes

DNA Sequence:
GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTACTTCTGTTTCCCC TTACTGCTTTTCCGATGGATGGAGATCAACCTGCAGACCAACCTGCAGATCGTATGC AGGACGACATTTCATCTGAGCAGTATCCCTTGTTTGATAAGAGACAAAAGTGTTGCA CTGGGAGGAAGGGGTCATGCTCCGGCAAAGCATGCAAAAATCTCAAATGTTGCTCT GGACGATAACGTGTTGATGACCAACTTTCTCGAN (SEQ ID NO:264)

Translation:
MMSKLGVLLTICLLLFPLTAFPMDGDQPADQPADRMQDDISSEQYPLFDKRQKCCTGR KGSCSGKACKNLKCCSGR (SEQ ID NO:265)

Toxin Sequence:
Xaa2-Lys-Cys-Cys-Thr-Gly-Arg-Lys-Gly-Ser-Cys-Ser-Gly-Lys-Ala-Cys-Lys-Asn-Leu-Lys-Cys-Cys-Ser-# (SEQ ID NO:266)

Name: Bt3.5
Species: betulinus
Cloned: Yes

DNA Sequence:
GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCC TTACTGCTGTTCCGTTGGATGGAGATCAACCTGCAGACCAACCTGCAGAGCGTATGC AGAACGAGCAGCATCCCTCGTTTGATCAGAAAAGAAGGTGCTGCCGGTGGCCATGC CCCAGTATATGCGGCATGGCTAGGTGTTGCTTCGTCATGATAACGTGTTGATGACCA ACTTTCTCGAG (SEQ ID NO:267)

Translation:
MMSKLGVLLTICLLLFPLTAVPLDGDQPADQPAERMQNEQHPSFDQKRRCCRWPCPSIC GMARCCFVMITC (SEQ ID NO:268)

Toxin Sequence:
Arg-Cys-Cys-Arg-Xaa4-Xaa3-Cys-Xaa3-Ser-Ile-Cys-Gly-Met-Ala-Arg-Cys-Cys-Phe-Val-Met-Ile-Thr-Cys-^ (SEQ ID NO:269)

Name: Bt3.6
Species: betulinus
Cloned: Yes

DNA Sequence:
GGATCCATGATGTCTAAACTGGGAGTCTTGTTGATCATCTGTCTGCTTCTGTTTCCCC
TTACTGCTGTTCCGCTGGATGGAGATCAGCCTGCAGAGCGTACGCAGATCGAGCAG
CATCCCTTGTTTGACCAGAAAAGAAGGTGTTGCCGGTGGCCATGCCCCAGTAGATG
CGGCATGGCTAGGTGTTGCTTCGTCATGATAACGTGTTGATGANCGACCTCTCNAG
(SEQ ID NO:270)

Translation:
MMSKLGVLLIICLLLFPLTAVPLDGDQPAERTQIEQHPLFDQKRRCCRWPCPSRCGMAR
CCFVMITC (SEQ ID NO:271)

Toxin Sequence:
Arg-Cys-Cys-Arg-Xaa4-Xaa3-Cys-Xaa3-Ser-Arg-Cys-Gly-Met-Ala-Arg-Cys-Cys-Phe-Val-Met-Ile-Thr-Cys-^ (SEQ ID NO:272)

Name: Pr3.1
Species: parius
Cloned: Yes

DNA Sequence:
GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCC
TTACTGCTCTTCCGATGGATGGTGATCAACCTGCAGACCGACTTGTAGAGCGTATGC
AGGACAACATTTCATCTGAGCAGCATCCCTTCTTTGAAAAGAGAAGAGGAGGCTGT
TGCACACCTCCGAAGAAATGCAAAGACCGAGCCTGCAAACCTGCACGTTGCTGCGG
CCCAGGATAACGTGTTGATGACCAACTTTCTCGCC (SEQ ID NO:273)

Translation:
MMSKLGVLLTICLLLFPLTALPMDGDQPADRLVERMQDNISSEQHPFFEKRRGGCCTPP
KKCKDRACKPARCCGPG (SEQ ID NO:274)

Toxin Sequence:
Arg-Gly-Gly-Cys-Cys-Thr-Xaa3-Xaa3-Lys-Lys-Cys-Lys-Asp-Arg-Ala-Cys-Lys-Xaa3-Ala-Arg-Cys-Cys-Gly-Xaa3-# (SEQ ID NO:275)

Name: Pr3.2
Species: parius
Cloned: Yes

DNA Sequence:
GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCC TTACTGCTCTTCCGATGGATGGTGATCAACCTGCAGACCGACTTGTAGAGCGTATGC AGGACAACATTTCATCTGAGCAGCATCCCTTCTTTGAAAAGAGAAGAGGCTGTTGC ACACCTCCGAGGAAATGCAAAGACCGAGCCTGCAAACCTGCACGTTGTTGCGGCCC AGGATAACGTGTTGATGACCAACTTTCTCGAG (SEQ ID NO:276)

Translation:
MMSKLGVLLTICLLLFPLTALPMDGDQPADRLVERMQDNISSEQHPFFEKRRGCCTPPR KCKDRACKPARCCGPG (SEQ ID NO:277)

Toxin Sequence:
Arg-Gly-Cys-Cys-Thr-Xaa3-Xaa3-Arg-Lys-Cys-Lys-Asp-Arg-Ala-Cys-Lys-Xaa3-Ala-Arg-Cys-Cys-Gly-Xaa3-# (SEQ ID NO:278)

Name: Ct3.1
Species: coronatus
Cloned: Yes

DNA Sequence:
GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCAA TTACTGCCCTTCCGCTGGATGAAGATCAACCTGCAGACCGACCTGCAGAGCGTATGC AGGACATTGCAACTGAACAGCATCCCTTGTTTGATCCCGTCAAACGGTGCTGCGATT GGCCATGCATCCCAGGATGCACCCCTTGTTGCTTGCCTTGATAACGTGTTGATGACC AACTTTCTCGAG (SEQ ID NO:279)

Translation:
MMSKLGVLLTICLLLFPITALPLDEDQPADRPAERMQDIATEQHPLFDPVKRCCDWPCIP GCTPCCLP (SEQ ID NO:280)

Toxin Sequence:
Cys-Cys-Asp-Xaa4-Xaa3-Cys-Ile-Xaa3-Gly-Cys-Thr-Xaa3-Cys-Cys-Leu-Xaa3-^ (SEQ ID NO:281)

Name: Ms3.1
Species: musicus
Cloned: Yes

DNA Sequence:
GGATCCATGATGTCTAAACTGGGAGTCCTGTTGACCATCTGTCTGCTTCTGTTTCCTC TTTCTGCTCTTCCGATGGATGAAGATCAACTTGCAGACCTACCTGCAGAGCGTATGC

GGGACACTGCAACTGTAGATCATCCCTCCTATGATCCTGACAAAGCGTGCTGCGAG CAGAGCTGTACAACATGCTTTCCGTGCTGCTAGCCTTGAACACAGTAACGTGTTGAT GACCAACTTTCTCGAG (SEQ ID NO:282)

Translation:
MMSKLGVLLTICLLLFPLSALPMDEDQLADLPAERMRDTATVDHPSYDPDKACCEQSC TTCFPCC (SEQ ID NO:283)

Toxin Sequence:
Ala-Cys-Cys-Xaa1-Gln-Ser-Cys-Thr-Thr-Cys-Phe-Xaa3-Cys-Cys-^ (SEQ ID NO:284)

Name: bt3b
Species: betulinus
Isolated: Yes

Toxin Sequence:

Ala-Cys-Cys-Xaa1-Gln-Ser-Cys-Thr-Thr-Cys-Met-Xaa3-Cys-Cys-^ (SEQ ID NO:285)

Name: bt3c
Species: betulinus
Isolated: Yes

Toxin Sequence:
Cys-Cys-Xaa1-Gln-Ser-Cys-Thr-Thr-Cys-Met-Xaa3-Cys-Cys-Xaa4-? (SEQ ID NO:286)

Name: Pn3.2
Species: pennaceus
Cloned: Yes

DNA Sequence:
GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCC TTACTGCTCTTCCGCTGGATGGAGATCAACCTGCATACCAAGCTGCAGAGCGTATGC AGGCCGAGCATCATCCCTTGTTTGATCAGAAAAGACGGTGCTGCAAGTTTCCATGCC CCGATAGTTGCAAATATTTGTGTTGCGGGTGATGATAACATGTTGATGACCAACTTT CTTGAG (SEQ ID NO:287)

Translation:
MMSKLGVLLTICLLLFPLTALPLDGDQPAYQAAERMQAEHHPLFDQKRRCCKFPCPDS CKYLCCG (SEQ ID NO:288)

Toxin Sequence:
Arg-Cys-Cys-Lys-Phe-Xaa3-Cys-Xaa3-Asp-Ser-Cys-Lys-Xaa5-Leu-Cys-Cys-# (SEQ ID NO:289)

Name: Pu3.2
Species: pulicarius
Cloned: Yes

DNA Sequence:
GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCC
TTACTGCTCTTCCGATGGATGGTGATCAACTTGCAGACCGACTTGTAGAGCGTATGC
AGGACAACATTTCATCTGAGCAGCATCCCTTCTTTGATCCCGTCAAACGGTGTTGCG
TCAGCTGTTACATGGGATGCATCCCTTGTTGCTTCTAGTAATAACGTGTTGATGACC
AACTTTCTCGAG (SEQ ID NO:290)

Translation:
MMSKLGVLLTICLLLFPLTALPMDGDQLADRLVERMQDNISSEQHPFFDPVKRCCVSCY
MGCIPCCF (SEQ ID NO:291)

Toxin Sequence:
Cys-Cys-Val-Ser-Cys-Xaa5-Met-Gly-Cys-Ile-Xaa3-Cys-Cys-Phe-^ (SEQ ID NO:292)

Name: Pu3.3
Species: pulicarius
Cloned: Yes

DNA Sequence:
GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCGTCTGTCTGCTTCTGTGTCCCC
TTACTGCTCTTCCACTGGATGAAGATCAACTTGCAGACCGACCTGCAGAGCGTATGC
AGGATGACACTTCAGCTGCACAGATTTTCGGGTTTGATCCCGTCAAACGGTGCTGCA
AATTGCTATGCTACTCGGGATGCACTCCTTGTTGCCATATTTGATAACGTGTTGATG
ACCAACTTTCTCGAG (SEQ ID NO:293)

Translation:
MMSKLGVLLTVCLLLCPLTALPLDEDQLADRPAERMQDDTSAAQIFGFDPVKRCCKLL
CYSGCTPCCHI (SEQ ID NO:294)

Toxin Sequence:
Cys-Cys-Lys-Leu-Leu-Cys-Xaa5-Ser-Gly-Cys-Thr-Xaa3-Cys-Cys-His-Ile-^ (SEQ ID NO:295)

Name: Ra3.2
Species: rattus
Cloned: Yes

DNA Sequence:
GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTGTGTTTCCGC
TTACTGCTCTTCCGATGGATGGTGATCAACCTGCAGACCGACTTGTAGAGCGTATAC

AGGACAACATTTCATCTGAGCAGCATCCCTTCTTTGAAAAGAGAAGAGGCTGTTGC
GCACCTCCGAGGAAATGCAAAGACCGAGCCTGCAAACCTGCACGTTGCTGCGGCCC
AGGATAACGTGTTGATGACCAACTTTCTCGAG (SEQ ID NO:296)

Translation:
MMSKLGVLLTICLLVFPLTALPMDGDQPADRLVERIQDNISSEQHPFFEKRRGCCAPPRK
CKDRACKPARCCGPG (SEQ ID NO:297)

Toxin Sequence:
Arg-Gly-Cys-Cys-Ala-Xaa3-Xaa3-Arg-Lys-Cys-Lys-Asp-Arg-Ala-Cys-Lys-Xaa3-Ala-Arg-Cys-Cys-Gly-Xaa3-# (SEQ ID NO:298)

Name: Sm3.3
Species: stercusmuscarum
Cloned: Yes

DNA Sequence:
GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACAATCTGTCTGCTTCTGTTTCCCC
TTATTGCTCTTCCGCTGGATGGAGATCAACCTGCAGACCGACCTGCAGAGCGTATGC
AGGACGACATTTCATCTGAGAAGCATCCCTTGTTTGATAAGAGACAACGGTGTTGC
AATGGGCGGAGGGGATGCTCCAGCAGATGGTGCAGAGATCACTCACGTTGTTGCGG
TCGACGATAACGTGTTGATGACCAACTTTCTCGAG (SEQ ID NO:299)

Translation:
MMSKLGVLLTICLLLFPLIALPLDGDQPADRPAERMQDDISSEKHPLFDKRQRCCNGRR
GCSSRWCRDHSRCCGRR (SEQ ID NO:300)

Toxin Sequence:
Xaa2-Arg-Cys-Cys-Asn-Gly-Arg-Arg-Gly-Cys-Ser-Ser-Arg-Xaa4-Cys-Arg-Asp-His-Ser-Arg-Cys-Cys-# (SEQ ID NO:301)

Name: Eb3.1
Species: ebraeus
Cloned: Yes

DNA Sequence:
GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCC
TTACTGCTCTTCCACTGGATGAAGGTCAACCTGCAGACCTACCTGCAGAGCGTATGC
AGGACATTGCAACTGAACAGCATCCCTTGTTTGATCCTGTCAAACGGTGTTGCGAGC
AGCCATGCTACATGGGATGCATCCCTTGTTGCTTCTAATAATAACGTGTTGATGACC
AACTTTCTCGAG (SEQ ID NO:302)

Translation:
MMSKLGVLLTICLLLFPLTALPLDEGQPADLPAERMQDIATEQHPLFDPVKRCCEQPCY
MGCIPCCF (SEQ ID NO:303)

Toxin Sequence:
Cys-Cys-Xaa1-Gln-Xaa3-Cys-Xaa5-Met-Gly-Cys-Ile-Xaa3-Cys-Cys-Phe-^ (SEQ ID NO:304)

Name: Eb3.2
Species: ebraeus
Cloned: Yes

DNA Sequence:
GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCC
TTACTGCTCTTCCACTGGATGAAGATCAACCTGCAGACCTACCTGCAGAGCGTATGC
AGGACATTGCAACTGAACAGCATCCCTTGTTTGATCCTGTCAAACGGTGCTGCGCGC
AGCCATGCTACATGGGATGCATCCCTTGTTGCTTCTAATAATAACGTGTTGATGACC
AACTTTCTCGAG (SEQ ID NO:305)

Translation:
MMSKLGVLLTICLLLFPLTALPLDEDQPADLPAERMQDIATEQHPLFDPVKRCCAQPCY
MGCIPCCF (SEQ ID NO:306)

Toxin Sequence:
Cys-Cys-Ala-Gln-Xaa3-Cys-Xaa5-Met-Gly-Cys-Ile-Xaa3-Cys-Cys-Phe-^ (SEQ ID NO:307)

Name: Fd3.2
Species: flavidus
Cloned: Yes

DNA Sequence:
GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCC
TTACTGCTGTTCCGTTGGATGGAGATCAACCTGCAGACCAGCCTGCAGAGCGTATGC
AGAACGAGCAGCATCCCTTGTTTGATCAGAAAAGAAGGTGCTGCCGGTGGCCATGC
CCCAGTATATGCGGCATGGCTAGGTGTTGCTCGTCATGATAACGTGTTGATGACCAA
CTTTCTCGAG (SEQ ID NO:308)

Translation:
MMSKLGVLLTICLLLFPLTAVPLDGDQPADQPAERMQNEQHPLFDQKRRCCRWPCPSIC
GMARCCSS (SEQ ID NO:309)

Toxin Sequence:
Arg-Cys-Cys-Arg-Xaa4-Xaa3-Cys-Xaa3-Ser-Ile-Cys-Gly-Met-Ala-Arg-Cys-Cys-Ser-Ser-^
(SEQ ID NO:310)

Name: Mf3.1
Species: miliaris
Cloned: Yes

DNA Sequence:
GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCAA TTACTGCCCTTCCACTGGATGAAGATCAACCTGCAGACCGACCTGCAGAGCGTATGC AGGACATTGCAACTGAACAGCATCCCTTGTTTGATCCCGTCAAACGGTGTTGCGATT GGCCATGCAGCGCAGGATGCTACCCTTGTTGCTTCCCTTAATAACGTGTTGATGACC AACTNANGNAAAAAAA (SEQ ID NO:311)

Translation:
MMSKLGVLLTICLLLFPITALPLDEDQPADRPAERMQDIATEQHPLFDPVKRCCDWPCS AGCYPCCFP (SEQ ID NO:312)

Toxin Sequence:
Cys-Cys-Asp-Xaa4-Xaa3-Cys-Ser-Ala-Gly-Cys-Xaa5-Xaa3-Cys-Cys-Phe-Xaa3-^ (SEQ ID NO:313)

Name: Mf3.2
Species: miliaris
Cloned: Yes
Notes:

DNA Sequence:
GGATCCATGATGTCTAAACTGGGAGTGGTGCCATTCGTCTTTCTGGTCCTGTTTCCCC TGGCAACACTCCAACTGGATGCAGATCAACCTGCAGACCGACCTGCGCGTAAAAAG GGCATTGCAACTAAACGGCATCCCTTGTCTGATCCTGTCAGAGGGTGTTGCCCTCCA ATGTGCACACCATGCTTCCCTTGCTGTTTTCGTTAATAACGTGTTGATGNATGATGN AN (SEQ ID NO:314)

Translation:
MMSKLGVVPFVFLVLFPLATLQLDADQPADRPARKKGIATKRHPLSDPVRGCCPPMCTPCFPCC FR (SEQ ID NO:315)

Toxin Sequence:
Gly-Cys-Cys-Xaa3-Xaa3-Met-Cys-Thr-Xaa3-Cys-Phe-Xaa3-Cys-Cys-Phe-Arg-^ (SEQ ID NO:316)

Name: Af3.1
Species: ammiralis
Cloned: Yes

DNA Sequence:
CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG TCTGCTTCTGTTTCCCCTTACTGCTCTTCCGCTGGATGGAGATCAACCTGCAGACCA AGCTGCAGAGCGTATGCAGGCCGAGCAGCATCCCTTGTTTGATCAGAAAAGACGGT GTTGCAGGTTTCCATGCCCCGATACTTGCAGACATTTGTGTTGCGGGTGATGATAAC

GTGCTGATGACCCACTTTGTCATCACGGCTACGTCAAGTGTCTAATGAATAAGTAAA ATGATTGCAGT (SEQ ID NO:317)

Translation:
MMSKLGVLLTICLLLFPLTALPLDGDQPADQAAERMQAEQHPLFDQKRRCCRFPCPDT CRHLCCG (SEQ ID NO:318)

Toxin Sequence:
Arg-Cys-Cys-Arg-Phe-Xaa3-Cys-Xaa3-Asp-Thr-Cys-Arg-His-Leu-Cys-Cys-# (SEQ ID NO:319)

Name: Af3.2
Species: ammiralis
Cloned: Yes

DNA Sequence:
CAAGAGGGATCGATAGCAGTTCATGATGTTTAAACTGGGAGTCTTGCTGACCATCTG TCTACTTCTGTTTTCCCTTAATGCTGTTCCGCTGGATGGAGATCAACCTGCAGACCA ACCTGCAGAGCGTCTGCTGGACGACATTTCATCTGAAAATAATCCCTTTTATGATCC CGCCAAACGGTGTTGCATGACTTGCTTCGGTTGCACACCTTGTTGTGGATGACCAGC CTCATCAAGTGTCTAACGAATAAGTAAAACGATTGCAGT (SEQ ID NO:320)

Translation:
MMFKLGVLLTICLLLFSLNAVPLDGDQPADQPAERLLDDISSENNPFYDPAKRCCMTCF GCTPCCG (SEQ ID NO:321)

Toxin Sequence:
Cys-Cys-Met-Thr-Cys-Phe-Gly-Cys-Thr-Xaa3-Cys-Cys-# (SEQ ID NO:322)

Name: Af3.3
Species: ammiralis
Cloned: Yes

DNA Sequence:
CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGCCTTGTTGACCATCT GTCTACTTCTGTTTTCCCTTACTGCTGTTCCGCTGGATGGAGATCAACATGCAGACC AACCTGCAGAGCGTCTGCAGGACCGCCTTCCAACTGAAAATCATCCCTTATATGATC CCGTCAAACGGTGTTGCGATGATTCGGAATGCGACTATTCTTGCTGGCCTTGCTGTA TTTTTTCATAACCTTTGTTATCGCGGCCTCATCCTAGTGTCAAATGAATAAGTAAAA CGATTGCAGT (SEQ ID NO:323)

Translation:
MMSKLGALLTICLLLFSLTAVPLDGDQHADQPAERLQDRLPTENHPLYDPVKRCCDDSE CDYSCWPCCIFS (SEQ ID NO:324)

Toxin Sequence:
Cys-Cys-Asp-Asp-Ser-Xaa1-Cys-Asp-Xaa5-Ser-Cys-Xaa4-Xaa3-Cys-Cys-Ile-Phe-Ser-^ (SEQ ID NO:325)

Name: Af3.4
Species: ammiralis
Cloned: Yes

DNA Sequence:
CAAGAGGGATCGATAGCAGTTCATGATGTTTAAACTCGGAGTCTTGCTGACCATCTG
TCTACTTCTGTTTTCCCTAATtGCTGTTCCGCTGGATGGAGATCAACATGCAGACCAA
CCTGCAGAGCGTCTGCAGGACCGCCTTCCAACTGAAAATCATCCCTTATATGATCCC
GTCAAACGGTGTTGCAGGTTGTTATGCCTCAGTTGCAACCCTTGTTGTGGATGACCA
GCTTTGTTATCACGGCCTCATCAAGTGTCTAATGAATAAGTAAAACGATTGCAGT
(SEQ ID NO:326)

Translation:
MMFKLGVLLTICLLLFSLIAVPLDGDQHADQPAERLQDRLPTENHPLYDPVKRCCRLLC
LSCNPCCG (SEQ ID NO:327)

Toxin Sequence:
Cys-Cys-Arg-Leu-Leu-Cys-Leu-Ser-Cys-Asn-Xaa3-Cys-Cys-# (SEQ ID NO:328)

Name: Af3.6
Species: ammiralis
Cloned: Yes

DNA Sequence:
CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGCCTTGTTGACCATCT
GTCTACTTCTGTTTTCCCTTACTGCTGTTCCGCTGGATGGAGATCAACATGCAGACC
AACCTGCAGAGCGTCTGCAGGACCGCATTCCAACTGAAGATCATCCCTTATTTGATC
CCAACAAACGGTGTTGCGATGATTCGGAATGCGGCTATTCATGCTGGCCTTGCTGTT
ATGGATAAGCTTTGTTATCGCGGCCTCATCCAGTGTCAACGAATAAGTAAAACGATT
GCAGT (SEQ ID NO:329)

Translation:
MMSKLGALLTICLLLFSLTAVPLDGDQHADQPAERLQDRIPTEDHPLFDPNKRCCDDSE
CGYSCWPCCYG (SEQ ID NO:330)

Toxin Sequence:
Cys-Cys-Asp-Asp-Ser-Xaa1-Cys-Gly-Xaa5-Ser-Cys-Xaa4-Xaa3-Cys-Cys-Xaa5-# (SEQ ID NO:331)

Name: Sf3.1
Species: spurius
Cloned: Yes

DNA Sequence:
CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGCTGACCATCT GTCTGCTTCTGTTTCCACGTACTTCTCTTCCGCTGGATGGAGATCAACCTGCAGTCCG ATCTGCAAAGCGTATGCATTCATCTATACAGCGTCGTTTCTTTGATCCCGTCAAACG GTGTTGCCCTAGATGCAGCGAGTGCAACCCTTGTTGTGGATGACCAGCTTTGTCATC GCGGCCTCATTAAGTGTCTAATGAATAAGTAAAATGATTGCAGT (SEQ ID NO:332)

Translation:
MMSKLGVLLTICLLLFPRTSLPLDGDQPAVRSAKRMHSSIQRRFFDPVKRCCPRCSECNP CCG (SEQ ID NO:333)

Toxin Sequence:
Cys-Cys-Xaa3-Arg-Cys-Ser-Xaa1-Cys-Asn-Xaa3-Cys-Cys-# (SEQ ID NO:334)

Name: Om3.1
Species: omaria
Cloned: Yes

DNA Sequence:
CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTCGTTGACCATCT GTCTACTTCTATTTTCCCTTACTGCTGTTCCGCTTGATGGAGATCAACATGCAGACCA ACCTGCAGAGCGTCTGCAGGGCGACATTTTATCTGAAAAGCATCCCTTATTTAATCC CGTCAAACGGTGTTGCGATGAGGAAGAATGCAGCAGTGCATGCTGGCCTTGTTGTT GGGGGTGATCAGCTTTGTTATCGCGGCCTCATCAAGTGTCTAATGAATAAGTAAAAT GATTGCAGT (SEQ ID NO:335)

Translation:
MMSKLGVSLTICLLLFSLTAVPLDGDQHADQPAERLQGDILSEKHPLFNPVKRCCDEEE CSSACWPCCWG (SEQ ID NO:336)

Toxin Sequence:
Cys-Cys-Asp-Xaa1-Xaa1-Xaa1-Cys-Ser-Ser-Ala-Cys-Xaa4-Xaa3-Cys-Cys-Xaa4-# (SEQ ID NO:337)

Name: Om3.2
Species: omaria
Cloned: Yes

DNA Sequence:
CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGATCATCTG TCTACTTCTGTGTCCCCTTACTGCTGTTCTGGAGGATGGAGATCAACCTGCAGACCG

ACCTGCAGAGCGTATGCAGGACGACATTTCAACTGAGCATCATCCCTTTTATGATCC CGTCAAACGGTGTTGCAAGTACGGGTGGACATGCTTGCTAGGATGCACTCCTTGTGA TTGTTGACCAGTTTTGTTATCGCGGCCTCGTCAAGTGTCTAATGAATAAGTAAAACG ATTGCAGT (SEQ ID NO:338)

Translation:
MMSKLGVLLIICLLLCPLTAVLEDGDQPADRPAERMQDDISTEHHPFYDPVKRCCKYG WTCLLGCTPCDC (SEQ ID NO:339)

Toxin Sequence:
Cys-Cys-Lys-Xaa5-Gly-Xaa4-Thr-Cys-Leu-Leu-Gly-Cys-Thr-Xaa3-Cys-Asp-Cys-^ (SEQ ID NO:340)

Name: Om3.3
Species: omaria
Cloned: Yes

DNA Sequence:
CAAGAGGGATCGATAGCAGTTCATGATGTCTATACTGGGAGTCTTGTTGATCATCTG TCTACTTCTGTGTCCCCTTACTGCTGTTCTGGAGGATGGAGATCAACCTGCAGACCG ACCTGCAGAGCGTATGCAGGACGGCATTTCATCTGAACATCATCCCTTTTTGGATCC CGTCAAACGGTGTTGCCATCTATTGGCATGCCGCTTTGGATGCTCGCCTTGTTGTTG GTGACCAGCTTTGTTATCGCGGCCTCATCAAGTGTCTAATGAATAAGTAAAACGATT GCAGT (SEQ ID NO:341)

Translation:
MMSILGVLLIICLLLCPLTAVLEDGDQPADRPAERMQDGISSEHHPFLDPVKRCCHLLAC RFGCSPCCW (SEQ ID NO:342)

Toxin Sequence:
Cys-Cys-His-Leu-Leu-Ala-Cys-Arg-Phe-Gly-Cys-Ser-Xaa3-Cys-Cys-Xaa4-^ (SEQ ID NO:343)

Name: Om3.4
Species: omaria
Cloned: Yes

DNA Sequence:
CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGATCATCTG TCTACTTCTTTGTCCCCTTACTGCTGTTCCGCAGGATGGAGATCAACCTGCAGACCG ACCTGCAGAGCGTATGCAGGGCGGCATTTCATCTGAACATCATCCCTTTTTTGATCC CGTCAAACGGTGTTGCAGGTACGGGTGGACATGCTGGCTAGGATGCACTCCCTGTG GTTGTTGACCAGCTTTGTTATCGCGGCCTCATCAAGTGTCTAATGAATAAGTAAAAC GATTGCAGT (SEQ ID NO:344)

Translation:

MMSKLGVLLIICLLLCPLTAVPQDGDQPADRPAERMQGGISSEHHPFFDPVKRCCRYGW TCWLGCTPCGC (SEQ ID NO:345)

Toxin Sequence:
Cys-Cys-Arg-Xaa5-Gly-Xaa4-Thr-Cys-Xaa4-Leu-Gly-Cys-Thr-Xaa3-Cys-Gly-Cys-^ (SEQ ID NO:346)

Name: Ep3.1
Species: episcopatus
Cloned: Yes

DNA Sequence:
CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG TCTACTTCTGTTTTCCCTTATTGCTGTTCCGCTTGATGGAGATCAACATGCAGACCAA CCTGCAGAGCGTCTGCAGGGCGACATTTTATCTGAAAAGCATCCCTTATTTATGCCT GTCAAACGGTGTTGCGATGAGGACGAATGCAACAGTTCATGCTGGCCTTGTTGTTGG GGGTGATCAGCTTTGTTATCGCGGCCTGATCAAGTGTATAATGAATAAGTAAAACG ATTGCAGT (SEQ ID NO:347)

Translation:
MMSKLGVLLTICLLLFSLIAVPLDGDQHADQPAERLQGDILSEKHPLFMPVKRCCDEDE CNSSCWPCCWG (SEQ ID NO:348)

Toxin Sequence:
Cys-Cys-Asp-Xaa1-Asp-Xaa1-Cys-Asn-Ser-Ser-Cys-Xaa4-Xaa3-Cys-Cys-Xaa4-# (SEQ ID NO:349)

Name: Ep3.2
Species: episcopatus
Cloned: Yes

DNA Sequence:
CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG TCTACTTCTGTTTTCCCTTATTGCTGTTCCGCTTGATGGAGATCAACATGCAGACCAA CCTGCAGAGCGTCTGCAGGGCGACATTTTATCTGAAAAGCATCCCTTATTTATGCCT GTCAAACGGTGTTGCGATGAGGACGAATGCAGCAGTTCATGCTGGCCTTGTTGTTGG GGATGAGCAGCTTTGTTATCGCGGCCTCATCAAGTGTCTAATGAATAAGTAAAACG ATTGCAGT (SEQ ID NO:350)

Translation:
MMSKLGVLLTICLLLFSLIAVPLDGDQHADQPAERLQGDILSEKHPLFMPVKRCCDEDE CSSSCWPCCWG (SEQ ID NO:351)

Toxin Sequence:

Cys-Cys-Asp-Xaa1-Asp-Xaa1-Cys-Ser-Ser-Ser-Cys-Xaa4-Xaa3-Cys-Cys-Xaa4-# (SEQ ID NO:352)

Name: Ep3.3
Species: episcopatus
Cloned: Yes

DNA Sequence:
CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG
TCTACTTCTGTTTTCCCTTACTGCTGTTCCGCTTGATGGAGATCAACATGCAGACCAA
CCTGCAGAGCGTCTGCAGGGCGACATTTTATCTGAAAAGCATCCCTTATTTAATCCC
GTCAAACGGTGTTGCCCGGCGGCGGCATGTGCCATGGGATGCAAGCCTTGTTGTGG
ATGAGCAGCTTTGTTATCGTGGCCTCATCAAGTGTCTAATGAATAAGTAAAACGATT
GCAGT (SEQ ID NO:353)

Translation:
MMSKLGVLLTICLLLFSLTAVPLDGDQHADQPAERLQGDILSEKHPLFNPVKRCCPAAA
CAMGCKPCCG (SEQ ID NO:354)

Toxin Sequence:
Cys-Cys-Xaa3-Ala-Ala-Ala-Cys-Ala-Met-Gly-Cys-Lys-Xaa3-Cys-Cys-# (SEQ ID NO:355)

Name: Au3.2
Species: aulicus
Cloned: Yes

DNA Sequence:
CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG
TCTGCTTCTGTTTTCCGTTACTGCTCTTCCGCCGGATGGAGATCAACCTGCAGACCG
AGCTGCAGAGCGTAGGCAGGTCGAGCAGCATCCCGTGTTTGATCATGAAAGAGGGT
GTTGCTCGCCACCATGCCACAGTATTTGCGCTGCTTTCTGTTGCGGGTGATGATAAC
GTGTTGATGACCCACTTTGTCATCACGGCTGCGTCAAGTGTCTAATGAATAAGTAAA
ATGATTGCAGT (SEQ ID NO:356)

Translation:
MMSKLGVLLTICLLLFSVTALPPDGDQPADRAAERRQVEQHPVFDHERGCCSPPCHSIC
AAFCCG (SEQ ID NO:357)

Toxin Sequence:
Gly-Cys-Cys-Ser-Xaa3-Xaa3-Cys-His-Ser-Ile-Cys-Ala-Ala-Phe-Cys-Cys-# (SEQ ID NO:358)

Name: Au3.3
Species: aulicus
Cloned: Yes

DNA Sequence:
CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG TCTACTTCTGTTTTCCCTTACTGCTGTTCCGCTTGATGGAGATCAACATGCAGACCAA CCTGCAGAGCGTCTGCAGGGCGACATTTTATCTGAAAAGCATCCCTTATTTAATCCC GTCAAACGGTGTTGCCGACCGGTGGCATGTGCCATGGGATGCAAGCCTTGTTGTGG ATGAGCAGCTTTGTTATCGTGGCCTCATCAAGTGTCTAATGAATAAGTAAAATGATT GCAGT (SEQ ID NO:359)

Translation:
MMSKLGVLLTICLLLFSLTAVPLDGDQHADQPAERLQGDILSEKHPLFNPVKRCCRPVA CAMGCKPCCG (SEQ ID NO:360)

Toxin Sequence:
Cys-Cys-Arg-Xaa3-Val-Ala-Cys-Ala-Met-Gly-Cys-Lys-Xaa3-Cys-Cys-# (SEQ ID NO:361)

Name: Au3.4
Species: aulicus
Cloned: Yes

DNA Sequence:
CAAGAGGGATCGATAGCAGTTCaTGATGTCTAAACTGGGAGTCTTGTTGATCATCTG TCTACTTCTGTCTCCCCTTACTGCTGTTCCGCTGGATGGAGATCAACCTGCAGACCG ACCTGCAGAGCGTATGCAGGACGACATTTCATCTGAACATCAACCCATGTTTGATGC CATCAGACAGTGTTGCCCGGCGGTGGCATGCGCCATGGGATGCGAGCCTTGTTGTG GATGACCAGCTTTGTTATCGCGGCCTCATCAAGTGTCTAATGAATAAGTAAAATGAT TGCAGT (SEQ ID NO:362)

Translation:
MMSKLGVLLIICLLLSPLTAVPLDGDQPADRPAERMQDDISSEHQPMFDAIRQCCPAVA CAMGCEPCCG (SEQ ID NO:363)

Toxin Sequence:
Xaa2-Cys-Cys-Xaa3-Ala-Val-Ala-Cys-Ala-Met-Gly-Cys-Xaa1-Xaa3-Cys-Cys-# (SEQ ID NO:364)

Name: Ae3.1
Species: aureus
Cloned: Yes

DNA Sequence:
CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGCCTTGTTGACCATCT GTCTACTTCTGTTTTCCCTTACTGCTGTTCCGCTGGATGGAGATCAACATGCAGACC AACATGCAGAGCGTCTGCATGACCGCCTTCCAACTGAAAATCATCCCTTATATGATC CCGTCAAACGGTGTTGCGATGATTCGGAATGCGACTATTCTTGCTGGCCTTGCTGTA

TTTTTGGATAACCTTTGTTATCGCGGCCTCATCAAGTGTCAAATGAATAAGTAAAAC GATTGCAGT (SEQ ID NO:365)

Translation:
MMSKLGALLTICLLLFSLTAVPLDGDQHADQHAERLHDRLPTENHPLYDPVKRCCDDS ECDYSCWPCCIFG (SEQ ID NO:366)

Toxin Sequence:
Cys-Cys-Asp-Asp-Ser-Xaa1-Cys-Asp-Xaa5-Ser-Cys-Xaa4-Xaa3-Cys-Cys-Ile-Phe-# (SEQ ID NO:367)

Name: Ae3.2
Species: aureus
Cloned: Yes

DNA Sequence:
CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGCCTTGTTGACCATCT GTCTACTTCTGTTTTCCCTAACTGCTGTTCCGCTGGATGGAGATCAACATGCAGACC AACCTGCAGAGCGTCTGCAGGACCGCATTCCAACTGAAAATCATCCCTTATTTGATC CGAACAAACGGTGTTGCAATGATTGGGAATGCGACGATTCATGCTGGCCTTGCTGTT ATGGATAACCTTTGTTATCGCGGCCTCATCAAGTGTCAAATGAATAAGTAAAACGAT TGCAGT (SEQ ID NO:368)

Translation:
MMSKLGALLTICLLLFSLTAVPLDGDQHADQPAERLQDRIPTENHPLFDPNKRCCNDWE CDDSCWPCCYG (SEQ ID NO:369)

Toxin Sequence:
Cys-Cys-Asn-Asp-Xaa4-Xaa1-Cys-Asp-Asp-Ser-Cys-Xaa4-Xaa3-Cys-Cys-Xaa5-# (SEQ ID NO:370)

Name: Cn3.1
Species: consors
Cloned: Yes

DNA Sequence:
CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG TTTGCTTCTGTTTCCCCTTACTGCTCTTCCAATGGATGGAGATCAATCTGTAGACCGA CCTGCAGAGCGTATGCAGGACGACATTTCATCTGAGCTGCATCCCTTGTTCAATCAG AAAAGAATGTGTTGCGGCGAAGGTGCGCCATGCCCCAGCTATTTCAGAAACAGTCA GATTTGTCATTGTTGTTAAATGACAACGTGTCGATGACCAACTTCGTTATCACGACT AATGAATAAGTAAAATGATTGCAGT (SEQ ID NO:371)

Translation:

MMSKLGVLLTICLLLFPLTALPMDGDQSVDRPAERMQDDISSELHPLFNQKRMCCGEG APCPSYFRNSQICHCC (SEQ ID NO:372)

Toxin Sequence:
Met-Cys-Cys-Gly-Xaa1-Gly-Ala-Xaa3-Cys-Xaa3-Ser-Xaa5-Phe-Arg-Asn-Ser-Gln-Ile-Cys-His-Cys-Cys-^ (SEQ ID NO:373)

Name: Cn3.3
Species: consors
Cloned: Yes

DNA Sequence:
TAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG TCTGCTTCTGTTTCCCCTTATTGCTCTTCCAATGGATGGAGATCAACCTGCAGACCGA CCTGCAGAGCGTATGCAgGACGACATTTCATCTCAGCAGCATCCCTTGTTTGATAAG AGAGGCCGCTGTTGCGATGTGCCGAACGCATGCTCCGGCAGATGGTGCAGAGATCA CGCACAATGTTGCGGATGACGATAACGTGTTGATGACCAACTTTGTGATCACGGCTA CATCAAGTGAATAAGTAAAACGATTGCAGT (SEQ ID NO:374)

Translation:
MMSKLGVLLTICLLLFPLIALPMDGDQPADRPAERMQDDISSQQHPLFDKRGRCCDVPN ACSGRWCRDHAQCCG (SEQ ID NO:375)

Toxin Sequence:
Gly-Arg-Cys-Cys-Asp-Val-Xaa3-Asn-Ala-Cys-Ser-Gly-Arg-Xaa4-Cys-Arg-Asp-His-Ala-Gln-Cys-Cys-# (SEQ ID NO:376)

Name: Cn3.4
Species: consors
Cloned: Yes

DNA Sequence:
CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACTGTCTG TTTGCTTCTGTTTCCCCTTACTGCTCTTCCGATGGATGGAGATCAACCTGCAGACCAA CCTGCAGAGCGTATGCAGGACGACATTTCATCTGAGCAGCATCCCTTGTTTGATAAG AGACAAAGGTGTTGCACTGGGAAGAAGGGGTCATGCTCCGGTAAAGCATGCAAAA GTCTCAAATGTTGCTCTGGACGATAACGTGTTGATGACCAACTTTGTTATCACGGCT ACGTCAAGTGTCTAGTGAATAAGTAAAACGATTGCAGT (SEQ ID NO:377)

Translation:
MMSKLGVLLTVCLLLFPLTALPMDGDQPADQPAERMQDDISSEQHPLFDKRQRCCTGK KGSCSGKACKSLKCCSGR (SEQ ID NO:378)

Toxin Sequence:

Xaa2-Arg-Cys-Cys-Thr-Gly-Lys-Lys-Gly-Ser-Cys-Ser-Gly-Lys-Ala-Cys-Lys-Ser-Leu-Lys-Cys-Cys-Ser-# (SEQ ID NO:379)

Name: Em3.1
Species: emaciatus
Cloned: Yes

DNA Sequence:
CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGCTGACCATCTGTCTGCTTCTGTT
TCCCCTTACTGTTCTTCCGATGGATGGAGATCAACCTGCAGACCTACCTGCATTGCGTGCGCAGTTCTT
TGCACCTGAACATAGTCCCCGGTTTGACCCCGTCAAACGGTGCTGCTCGCGGGATTGCAGTGTTTGCAT
CCCTTGTTGCCCGTATGGATCACCTTGATTATTGCGGCCACGTCAAGTGTCTAATGAATAAGTAAAATG
ATTGCAGT (SEQ ID NO:380)

Translation:
MMSKLGVLLTICLLLFPLTVLPMDGDQPADLPALRAQFFAPEHSPRFDPVKRCCSRDCSVCIPCCPYGSP
(SEQ ID NO:381)

Toxin Sequence:
Cys-Cys-Ser-Arg-Asp-Cys-Ser-Val-Cys-Ile-Xaa3-Cys-Cys-Xaa3-Xaa5-Gly-Ser-Xaa3-^ (SEQ ID NO:382)

Where:
Xaa1 is Glu or γ-carboxy-Glu
Xaa2 is Gln or pyro-Glu
Xaa3 is Pro or hydroxy-Pro
Xaa4 is Trp or bromo-Trp
Xaa5 is Tyr, ^{125}I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
^ is free carboxyl or amidated C-terminus, preferably free carboxyl
# is free carboxyl or amidated C-terminus, preferably amidated
? = Status of C-term not known.

TABLE2

Alignment of μ-Conopeptides (SEQ ID NO:)

TYPE 1

A3.4 (F283)	---CCKVQ-CES--C---TPCC^ (383)
Ak3.1 (F585)	---CCELP-CGPGFC---VPCC^ (384)
Ar3.1	---CCERP-CNIG-C---VPCC^ (385)
Bn3.1 (F586)	---CCNWP-CSMG-C---IPCCYY^ (386)
Bt3.1	---CCELP-CH-G-C---VPCCWP^ (387)
Bt3.2	---CCGLP-CN-G-C---VPCCWPS^ (388)
Bt3.3	---CCSRN-CAV--C---IPCCPNWPA^ (389)
bt3a	---CCKQS-CTT--C---MPCCW^ (390)

bt3b	--ACCXQS-CTT--C---MPCC^ (391)
bt3c	---CCEQS-CTT--C---MPCCW? (392)
Ca3.3	R--CCRYP-CPDS-C--HGSCCYK^ (393)
Ca3.4	---CCPPVACNMG-C---KPCC# (394)
Ca3.5	---CCDDSECDYS-C---WPCCMF# (395)
Ca3.6 (F349)	---CCRR--CYMG-C---IPCCF^ (396)
Circling	---CCPPVACNMG-C---KPCCG^ (397)
Comatose/Death	SKQCCHLAACRFG-C---TOCCN^ (398)
Cp3.1 (F594)	S--CCR--DCGED-C---VGCCR^ (399)
Ct3.1 (Z726)	---CCDWP-CIPG-C---TPCCLP^ (400)
Da3.1	---CCDDSECDYS-C---WPCCILS^ (401)
Da3.2	Z-QCCPPVACNMG-C---EPCC# (402)
Da3.3	---CCNAGFCRFG-C---TPCCW^ (403)
Di3.1	Z--CCVHP-C-P--C---TPCCR^ (404)
Fi3.1	---CCPWP-CNIG-C---VPCC^ (405)
Fi3.2	---CCSKN-CAV--C---IPCCP^ (406)
Fi3.3	---CCRWP-CP-ARC---GSCCL^ (407)
Fi3.4	---CCELSRCL-G-C---VPCCTS^ (408)
Fi3.5	---CCELSKCH-G-C---VPCCIP^ (409)
Ge3.1 (F590)	Z--CCTF--CNFG-C---QPCCVP^ (410)
Ge3.2 (F343/Z734)	Z--CCTF--CNFG-C---QPCCLT^ (411)
Ge3.3 (F590	Z--CCTF--CNFG-C---QPCCVP^ (412)
Gm3.1	---CCDDSECDYS-C---WPCCMF# (413)
Gm3.2	G--CCHLLACRFG-C---SPCCW^ (414)
Gm3.3	---CCSWDVCDHPSC---T-CCG# (415)
La3.1	---CCDWP-CS-G-C---IPCC^ (416)
Lp3.1 (F340)	ZINCCPWP-CPST-C--RHQCCH^ (417)
Lv3.1 (F341)	ZINCCPWP-CPDS-C--HYQCCH^ (418)
Mr3.2	---CCRLS-CGLG-C---HPCC# (419)
Mr3.3	--ECCGSFACRFG-C---VPCCV^ (420)
Mr3.4	SKQCCHLPACRFG-C---TPCCW^ (421)
Mr3.5 (F286)	-MGCCPFP-CKTS-C--TTLCC# (422)
Ms3.1 (Z738)	--ACCEQS-CTT--C---FPCC^ (423)
Nb3.1 (F87)	---CCELP-CGPGFC---VPCC^ (424)
Pu3.1 (F339)	---CCN-S-CYMG-C---IPCCF^ (425)
Qc3.1 (F342)	ZR-CCQWP-CPGS-C----RCCRT# (426)
Qc3.2	ZR-CCRWP-CPGS-C----RCCRYR^ (427)
Qc3.3	R--CCRYP-CPDS-C--HGSCCYK^ (428)
QcIIIA	---CCSQD-CLV--C---IOCCPN# (429)
QcIIIB	---CCSRH-CWV--C---IOCCPN? (430)
Ra3.1 (F351)	Z-TCCS-N-CGED-C---DGCCQ^ (431)
Scratcher I	---CCR-T-C-FG-C---TOCC# (433)
Ts3.1 (F592)	---CCH-K-CYMG-C---IPCCI^ (434)
Ts3.2 (F345)	K--CCRPP-CAMS-C-GMARCCY^ (435)
Bt3.5 (Z495)	R--CCRWP-CPSI-C-GMARCCFVMITC^ (436)
Bt3.6 (Z497)	R--CCRWP-CP-SRC-GMARCCFVMITC^ (437)
Tx3.1	F--CCDSNWCHISDC----ECCY# (438)

U014	---CCHWNWCDHL-C----SCCGS^ (439)
U017	--DCCOLPACPFG-C---NOCC# (440)
U019	---CCAPSACRLG-C---ROCCR^ (441)
U020	---CCAOSACRLG-C---ROCCR^ (442)
U022	---CCAPSACRLG-C---RPCCR^ (443)
U024	--GCCGSFACRFG-C---VOCCV^ (444)
U031	---CCSWDVCDHPSC----TCC# (445)
U032 (F353)	R--CCKFP-CPDS-C--RYLCC# (446)
Ae3.1	---CCDDSECDYS-C---WPCCIF# (447)
Ae3.2	---CCNDWECDDS-C---WPCCY# (448)
Af3.1	R--CCR-FPCPDT-C---RHLCC# (449)
Af3.2	---CC--MTC-FG-C---TPCC# (450)
Af3.3	---CCDDSECDYS-C---WPCCIFS^ (451)
Af3.4	---CCR-LLC-LS-C---NPCC# (452)
Af3.6	---CCDDSECGYS-C---WPCCY# (453)
Au3.2	G--CCS-PPCHSI-C--AAFCC# (454)
Au3.3	---CCRPVACAMG-C---KPCC# (455)
Au3.4	Z--CCPAVACAMG-C---EPCC# (456)
Em3.1	---CCS-RDC-SV-C---IPCCPYGSP^ (457)
Ep3.1	---CCDEDECNSS-C---WPCCW# (458)
Ep3.2	---CCDEDECSSS-C---WPCCW# (459)
Ep3.3	---CCPAAACAMG-C---KPCC# (460)
Om3.1	---CCDEEECSSA-C---WPCCW# (461)
Om3.3	---CCHLLACRFG-C---SPCCW^ (462)
Sf3.1	---CC--PRC-SE-C---NPCC# (463)

TYPE 2

Pn3.2 (AA049)	-RCC--KFP-CPDS-C--KYLCC# (464)
Fd3.2 (Z831)	-RCC--RWP-CPSI-C-GMARCCSS^ (465)
Pu3.3 (AA405)	--CC--KLL-CYSG-C---TPCCHI^ (466)
Eb3.1 (Z821)	--CC--EQP-CYMG-C---IPCCF^ (467)
Eb3.2 (Z822)	--CC--AQP-CYMG-C---IPCCF^ (468)
Pu3.2 (AA403)	--CC--V-S-CYMG-C---IPCCF^ (469)
Mf3.1 (Z882)	--CC--DWP-CSAG-C---YPCCFP^ (470)
Mf3.2 (Z885)	-GCC--PPM-C-TP-C---FPCCFR^ (471)
Ra3.2 (AA414)	RGCCAPPRK-CKDRACK-PARCCGP# (472)
Sm3.3 (AA419)	ZRCCNGRRG-CSSRWCRDHSRCC# (473)
Cn3.3	GRCCDVPNA-CSGRWCRDHAQCC# (474)
Cn3.4	ZRCCTGKKGSCSGKACKSL-KCCS# (475)

TYPE 3

A3.1	-MCCGEGRKCPSYFRNSQICHCC^ (476)
A3.2 (F84)	--CCR--WPCPRQIDGEY-CGCCL# (477)
Bu3.5	-RCCGEGLTCPRYWKNSQICACC^ (478)
Ca3.1	--CCGPGGSCPVYFRDNFICGCC^ (479)

Cr3.1	RKCCGKDGPCPKYFKDNFICGCC^ (480)
E3.1	--CCS--WPCPRYSNGKLVCFCCL# (481)
M3.2	--CCGPGGSCPVYFRDNFICGCC^ (482)
M3.3	-MCCGESAPCPSYFRNSQICHCC^ (483)
M3.4	ZKCCGPGGSCPVYFTDNFICGCC^ (484)
M3.5	ZKCCGPGGSCPVYFRDNFICGCC^ (485)
S3.1	ZKCCGEGSSCPKYFKNNFICGCC^ (486)
U001	ZKCCS-GGSCPLYFRDRLICPCC^ (487)
U034	ZKCCGPGASCPRYFKDNFICGCC^ (488)
Cn3.1	-MCCGEGAPCPSYFRNSQICHCC^ (489)

<u>TYPE 4</u>

A3.3 (F83)	ZK--CCTGK---KGSCSGKACKNL-KCCS# (490)
A3.5 (Z488)	ZK--CCTGR---KGSCSGKACKNL-KCCS# (491)
Bu3.1	VTDRCCK----GKREC-GRWCRDHSRCC# (492)
Bu3.1A	VGDRCCK----GKRGC-GRWCRDHSRCC# (493)
Bu3.2	VGERCCK---NGKRGC-GRWCRDHSRCC# (494)
Bu3.3	IVDRCCN-KGNGKRGC-SRWCRDHSRCC# (495)
Bu3.4	VGLYCCRPKPNGQMMC-DRWCEKNSRCC# (496)
Ca3.2	-RD-CCTPP---KK-CKDRQCKPQ-RCCA# (497)
L3.1	GRD-CCTPP---RK-CRDRACKPQ-RCCG# (498)
L3.2	ZRL-CCGFP---KS-CRSRQCKPH-RCC# (499)
La3.2	-RD-CCTPP---KK-CRDRQCKPA-RCCG# (500)
La3.3	RPP-CCTYD---GS-CLKESCMRK-ACC# (501)
La3.3A	RPP-CCTYD---GS-CLKESCKRK-ACC# (502)
μ-GIIIA	-RD-CCTOO---KK-CKDRQCKOQ-RCCA# (503)
μ-GIIIB	-RD-CCTOO---RK-CKDRRCKOM-KCCA# (504)
μ-GIIIC	-RD-CCTOO---KK-CKDRRCKOL-KCCA# (505)
μ-PIIIA	ZRL-CCGFO---KS-CRSRQCKOH-RCC# (506)
M3.1	-RD-CCTPP---KK-CKDRQCKPQ-RCCA# (507)
Mr3.1	RGG-CCTPP---RK-CKDRACKPA-RCCGP# (508)
Nb3.2 (F582)	ZK--CCTGK---KGSCSGKACKNL-KCCS# (509)
Pr3.1 (Z500)	RGG-CCTPP---KK-CKDRACKPA-RCCGP# (510)
Pr3.2 (Z501)	-RG-CCTPP---RK-CKDRACKPA-RCCGP# (511)
R3.1	LOS-CCSLN---LRLCOVOACKRN-OCCT# (512)
R3.2	ZQR-CCTVK----RICOVOACRSK-OCCKS^ (513)
R3.3	RGG-CCTPP---RK-CKDRACKPA-RCCGP# (514)
Sm3.1	ZK--CCTGK---KGSCSGKACKNL-KCCS# (515)
T3.1	H-G-CCKGO---EG-CSSRECROQ-HCC# (516)
T3.2 (Y088)	H-G-CCEGP---KG-CSSRECRPQ-HCC# (517)
Wi3.1 (M548)	LPS-CCDFE----RLCVVPACIRH-QCCT# (518)

<u>Type 5</u>

Om3.2	CCKYGWTCLLGCTPCDC^ (519)

Om3.4	CCRYGWTCWLGCTPCGC^ (520)

Type 6

S3.2 (F352)	Z-NCCNGG-CSSKWCRDHARCC# (432)

EXAMPLE 3

Effect of Intrathecal Administration of μ-Conopeptides

[0087] Male C57 black mice (20-25g) are obtained from Charles River Laboratories. These mice and the animals are housed in a temperature controlled (23° ± 3° C) room with a 12 hour light-dark cycle with free access to food and water. All animals are euthanized in accordance with Public Health Service policies on the humane care of laboratory animals.

[0088] Intrathecal (it) drug injections are performed as described (Hylden and Wilcox, 1980). A μ-conopeptide or vehicle is administered in a volume of 5 μl. Duration of hind-limb paralysis is assessed. This experiment reveals that injection of μ-conopeptides into the intrathecal space of C57 black mice produced a paralysis of the animal. The animals in this experiment recovered fully.

EXAMPLE 4

Effect of μ-Conopeptides as a Local Anesthetic

[0089] Male Hartley guinea pigs (retired breeders) are obtained form Charles River Laboratories. The local anesthetic test is performed essentially as described (Bulbring and Wajda, 1945). On the day prior to test day, a patch on the back of the guinea pig is denuded of hair, first by shaving with electric clippers and subsequently with depilatory cream (Nair®). Depilatory cream is applied for five minutes and removed with a warm washcloth. The guinea pigs are dried and returned to their cages. On the following day, intradermal injections (0.1 ml vols) of lidocaine, bupivacaine, a μ-conopeptide or vehicle (0.5% cyclodextran) are made into the denuded patch. The injection produced a raised wheal on the surface of the skin which is circled with a felt-tipped pen. Typically, four injections are made on the back of each guinea pig. In some cases, guinea pigs are reused following at least one week of recovery and injecting into an unused portion of the skin. The stimulus consists of mild pin pricks (not hard enough to break the skin) with a 26G needle. The response is a localized skin twitch caused by contraction

of cutaneous muscles. A unit test consisted of six uniform pin pricks, 3-5 seconds apart, within the injected area. Unit scores range from 0 (complete anesthesia) to 6 (no anesthesia). For potency experiments, the unit test is repeated at each site at five minute intervals for 30 minutes, and unit test scores summed (with 36 representing no anesthesia to 0 representing complete anesthesia. For duration experiments, unit tests are performed as described over the course of several hours to days.

[0090] μ-Conopeptides of the present invention produce a potent and long lasting local anesthetic effect in the intracutaneous wheal test in the guinea pig. As expected, bupivacaine has a slightly longer duration thatn lidocaine, consistent with clinical observations.

EXAMPLE 5

Muscle Relaxant Effect of μ-Conopeptides in Anesthetized Monkeys

[0091] μ-Conopeptides are dissolved 0.9 percent saline at a concentration of 2 mg/ml. Rhesus monkeys are anesthetized with halothane, nitrous oxide and oxygen. The maintenance concentration of halothane is 1.0%. Arterial and venous catheters are placed in the femoral vessels for drug administration and recording of the arterial pressure. Controlled ventilation is accomplished via an endotrachael tube. Twitch and tetanic contractions of the tibialis arterior muscle are elicited indirectly via the sciatic nerve. Recordings of arterial pressure electrocardiogram (lead I), heart rate, and muscle function are made simultaneously. Four to six animals received each listed compound. Four additional animals received succinylcholine chloride or d-tubocurarine chloride as controls. It is seen that the tested μ-conopeptides generally provide similar or better results than those seen for succinylcholine chloride or d-tubocurarine chloride.

EXAMPLE 6

In vivo Activity of μ-Conopeptides in Pain Models

[0092] The anti-pain activity of μ-conopeptides is shown in several animal models. These models include the nerve injury model (Chaplan, et al., 1997), the nocioceptive response to s.c. formalin injection in rats (Codene, 1993) and an NMDA-induced persistent pain model (Liu, et al., 1997). In each of these models it is seen that the μ-conopeptides and μ-conopeptides derivatives have analgesic properties.

[0093] More specifically, this study evaluates the effect of intrathecal administration of μ-conopeptides in mice models of nocioceptive and neuropathic pain. For nocioceptive pain, the effect of the μ-conopeptides is studied in two different tests of inflammatory pain. The first is the formalin test, ideal because it produces a relatively short-lived, but reliable pain behavior that is readily quantified. There are two phases of pain behavior, the second of which is presumed to result largely from formalin-evoked inflammation of the hind paw. A μ-conopeptide is administered 10 minutes prior to injection of formalin. The number of flinches and/or the duration of licking produced by the injection is monitored. Since the first phase is presumed to be due to direct activation of primary afferents, and thus less dependent on long term changes in the spinal cord, μ-conopeptides are presumed to have greatest effect on the magnitude of pain behavior in the second phase.

[0094] The mechanical and thermal thresholds in animals that received an injection of complete Freund's adjuvant into the hind paw are also studied. This produces a localized inflammation including swelling of the hind paw and a profound decrease in mechanical and thermal thresholds, that are detected within 24 hours after injection. The changes in thresholds in rats that receive μ-conopeptides are compared with those of rats that receive vehicle intrathecal injections.

[0095] An important issue is whether the drugs are effective when administered after the pain model has been established, or whether they are effective only if used as a pretreatment. Clearly, the clinical need is for drugs that are effective after the pain has developed. To address this issue, animals are studied in which μ-conopeptides are administered repeatedly, after the inflammation (CFA) or nerve injury has been established. In these experiments, a μ-conopeptide is injected daily by the intrathecal (i.t.) route. The mechanical and thermal thresholds (measured, respectively, with von Frey hairs in freely moving animals and with the Hargreave's test, also in freely moving animals) are repeated for a 2 to 4 week period after the injury is induced and the changes in pain measured monitored over time.

EXAMPLE 7

Effect of μ-Conotoxins in a Pain Model

[0096] Analgesic activity of μ-conotoxins is also tested in pain models as follows.

[0097] Persistent pain (formalin test). Intrathecal (it) drug injections are performed as described by Hylden and Wilcox (1980). An μ-conopeptide or vehicle is administered in a

volume of 5 μl. Fifteen minutes after the i.t. injection, the right hindpaw is injected with 20 μl of 5% formalin. Animals are placed in clear plexiglass cylinders backed by mirrors to facilitate observation. Animals are closely observed for 2 minutes per 5 minute period, and the amount of time the animal spent licking the injected paw is recorded in this manner for a total of 45-50 minutes. Results are expressed as licking time in seconds per five minutes. At the end of the experiment, all animals are placed on an accelerating rotorod and the latency to first fall was recorded. μ-Conopeptides are found to be active in this model which is predictive of efficacy for treating neuropathic pain.

[0098] Acute pain (tail-flick). A μ-conopeptide or saline is administered intrathecally (i.t.) according to the method of Hylden and Wilcox (1980) in a constant volume of 5 μl. Mice are gently wrapped in a towel with the tail exposed. At various time-points following the i.t. injection, the tail is dipped in a water bath maintained at 54° C. and the time to a vigorous tail withdrawal is recorded. If there is no withdrawal by 8 seconds, the tail is removed to avoid tissue damage.

[0099] Neuropathic pain. The partial sciatic nerve ligation model is used to assess the efficacy of μ-conopeptides in neuropathic pain. Nerve injury is produced according to the methods of Malmberg and Basbaum (1998). Animals are anesthetized with a ketamine/xylazine solution, the sciatic nerve is exposed and tightly ligated with 8-0 silk suture around 1/3 to ½ of the nerve. In sham-operated mice the nerve is exposed, but not ligated. Animals are allowed to recover for at least 1 week before testing is performed. On the testing day, mice are placed in plexiglass cylinders on a wire mesh frame and allowed to habituate for at least 60 minutes. Mechanical allodynia is assessed with calibrated von Frey filaments using the up-down method as described by Chaplan et al. (1994), and the 50% withdrawal threshold is calculated. Animals that did not respond to any of the filaments in the series are assigned a maximal value of 3.6 grams, which is the filament that typically lifted the hindlimb without bending, and corresponds to approximately 1/10 the animal's body weight.

[0100] The data obtained demonstrate that μ-conopeptides have potent analgesic properties in three commonly used models of pain: acute, persistent/inflammatory and neuropathic pain models.

EXAMPLE 8

Activity of μ-Conopeptide S3.2 on Neuronal Sodium Channels

[0101] μ-Conopeptide S3.2 was tested for activity on sodium channels as follows. S3.2 was administered to mice by intracerbroventricular (ICV) injection. Administration of S3.2 in this manner caused mice to show a spectrum of activity that is charcteristic of all sodium channel blockers, including rapdi loss of righting reflex, coma-like inactivity and spastic uncontrolled limb movement. Following intrathecal (it) administration to mice, S3.2 causes rapid hindlimb paralysis that spreads to include the entire body over a course of 10-20 minutes followed by death, presumably due to respiratory paralysis. However, unlike classic μ-conopeptides, S3.2 has no significant activity following intravenous administration (iv) to mice. Classic μ-conopeptides, such as GIIIA and PIIIA, cause rapid paralysis and death following iv administration, indicating their activity at skeletal muscle sodium channels. To confirm the selectivity of S3.2, 80 nmol was administered iv to rats. The effect of S3.2 was measured on skeletal muscle contraction, blood pressure and heart rate. S3.2 was found to have no effect on any of these parameters. Controls were performed using classical μ-conopeptides, including Sm3.1, Sm3.3 and Bu3.1 described herein, also administered iv at 80 nmol. These control peptides caused a dramatic decrease in skeletal muscle contractility, as well as a significant drop in systemic blood pressure. Thus, μ-conopeptide S3.2 suprisingly is selective for neuronal sodium channels. The most obvious difference between the S3.2 sequence and the sequences of these other peptides is a shortened first loop (the first loop between cysteine residues) which lacks a charged amino acid.

[0102] It will be appreciated that the methods and compositions of the instant invention can be incorporated in the form of a variety of embodiments, only a few of which are disclosed herein. It will be apparent to the artisan that other embodiments exist and do not depart from the spirit of the invention. Thus, the described embodiments are illustrative and should not be construed as restrictive.

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WHAT IS CLAIMED IS:

1. An isolated peptide selected from the group consisting of:
   (a) a peptide set forth in Table1 or Table 2 and
   (b) a derivative of the peptide in (a).

2. The isolated peptide of claim 1, wherein Xaa_1 is Glu, Xaa_2 is pyro-Glu, Xaa_4 is Trp and Xaa_5 is Tyr.

3. The derivative of the peptide of claim 1, in which the Arg residues may be substituted by Lys, ornithine, homoargine, nor-Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any synthetic basic amino acid; the Lys residues may be substituted by Arg, ornithine, homoargine, nor-Lys, or any synthetic basic amino acid; the Tyr residues may be substituted with meta-Tyr, ortho-Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any synthetic hydroxy containing amino acid; the Ser residues may be substituted with Thr or any synthetic hydroxylated amino acid; the Thr residues may be substituted with Ser or any synthetic hydroxylated amino acid; the Phe residues may be substituted with any synthetic aromatic amino acid; the Trp residues may be substituted with Trp (D), neo-Trp, halo-Trp (D or L) or any aromatic synthetic amino acid; the Asn, Ser, Thr or Hyp residues may be glycosylated;. the Tyr residues may also be substituted with the 3-hydroxyl or 2-hydroxyl isomers (meta-Tyr or ortho-Tyr, respectively) and corresponding O-sulpho- and O-phospho-derivatives; the acidic amino acid residues may be substituted with any synthetic acidic amino acid, e.g., tetrazolyl derivatives of Gly and Ala; the aliphatic amino acids may be substituted by synthetic derivatives bearing non-natural aliphatic branched or linear side chains C_nH_{2n+2} up to and including n=8; the Met residues may be subsituted by Nle; the Cys residues may be in D or L configuration and may optionally be substituted with homocysteine (D or L); pairs of Cys residues may be replaced pairwise with isoteric lactam or ester-thioether replacements, such as Ser/(Glu or Asp), Lys/(Glu or Asp), Cys/Glu (or Asp) or Cys/Ala combinations; and the peptide may be radioiodinated or radiotriated.

4. A substantially pure μ-conotoxin peptide derivative comprising a permutant of the peptide of claim 1,2 or 3.

5. A substantially pure μ-conotoxin peptide derivative comprising the peptide or peptide derivative of claim 1, 2 or 3 modified to contain an O-glycan, an S-glycan or an N-glycan.

6. A substantially pure μ-conotoxin peptide derivative comprising the peptide derivative of claim 4 modified to contain an O-glycan, an S-glycan or an N-glycan.

7. An isolated nucleic acid encoding a μ-conopeptide propeptide having an amino acid sequence set forth in Table 1.

8. The isolated nucleic acid of claim 7, wherein the nucleic acid comprises a nucleotide sequence set forth in Table 1.

9. An isolated μ-conopeptide propeptide having an amino acid sequence set forth in Table 1.

10. A method for treating or preventing disorders associated with voltage gated ion channel disorders in which comprises administering to a patient in need thereof a therapeutically effective amount of a peptide of claim 1 or a pharmaceutically acceptible salt thereof.

11. The method of claim 10, wherein said disorder is a neurologic disorder.

12. The method of claim 11, wherein said neurologic disorder is Amytrophic Lateral Sclerosis.

13. The method of claim 11, wherein said neurologic disorder is head trauma.

14. The method of claim 11, wherein said neurologic disorder is epilepsy.

15. The method of claim 11, wherein said neurologic disorder is a neurotoxic injury associated with conditions of hypoxia, anoxia or ischemia.

16. The method of claim 15, wherein said neurotoxic injury is associated with stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, drownings, suffocation, perinatal asphyxia, or hypoglycemic events.

17. The method of claim 10, wherein said disorder is pain.

18. The method of claim 17, wherein said pain is migraine, acute pain, persistent pain, chronic pain, neuropathic pain or nociceptive pain.

19. The method of claim 18, wherein the pain is trigeminal neuralgia, diabetic neuropathy, post-herpetic neuralgia, neuroma pain, phantom limb pain.

20. The method of claim 17, wherein said pain is burn pain.

21. The method of claim 10, wherein said disorder is a neuromuscular disorder.

22. The method of claim 21, wherein said neuromuscular disorder is myofacial pain syndrome, chronic muscle spasm, dystonias or spasticity.

23. A method for providing musculoskeletal relaxation in a patient undergoing a surgical procedure requiring anesthesia which comprises administering to a patient in need thereof a therapeutically effective amount of a peptide of claim 1 or a pharmaceutically acceptible salt thereof.

24. A method of alleviating pain which comprises administering to a mammal that is either exhibiting pain or is about to be subjected to a pain-causing event a pain-alleviating amount of a peptide of claim 1 or a pharmaceutically acceptible salt thereof.

25. The method of claim 24, wherein the peptide is administered as a local anesthetic.

26. The method of claim 24, wherein the peptide is administered as an occular anesthetic.

27. A method for characterizing a pore occlusion site on a sodium channel subtype comprising determining the affinity of said site for a peptide of claim 1.

28. The method of claim 27, wherein said sodium channel subtype is a neuronal sodium channel subtype and said peptide is μ-conopeptide S3.2 comprising an amino acid sequence as set forth in SEQ ID NO:211 or SEQ ID NO:432.

29. A method for screening a small molecule library to identify a small molecule which is a selective blocking agent of a sodium channel subtype comprising (a) measuring the blocking activity of a small molecule on said sodium channel subtype, (b) measuring the blocking activity of a peptide of claim 1 on said sodium channel subtype and (c) comparing the blocking activity of said small molecule with the blocking activity of said peptide.

30. The method of claim 29, wherein said sodium channel subtype is a neuronal sodium channel subtype and said peptide is μ-conopeptide S3.2 comprising an amino acid sequence as set forth in SEQ ID NO:211 or SEQ ID NO:432.

31. A method for screening a small molecule library to identify a small molecule which is a selective blocking agent of a sodium channel subtype comprising (a) measuring the binding affinity of a small molecule on said sodium channel subtype, (b) measuring the binding affinity of a peptide of claim 1 on said sodium channel subtype and (c) comparing the binding affinity of said small molecule with the binding affinity of said peptide.

32. The method of claim 31, wherein said peptide is radiolabeled.

33. The method of claim 31, wherein said sodium channel subtype is a neuronal sodium channel subtype and said peptide is μ-conopeptide S3.2 comprising an amino acid sequence as set forth in SEQ ID NO:211 or SEQ ID NO:432.

34. The method of claim 33, wherein said peptide is radiolabeled.

35. A method for screening a small molecule library to identify a small molecule which is a selective blocking agent of a sodium channel subtype comprising (a) allowing a peptide of claim 1 to bind to a sodium channel subtype, (b) adding a small molecule and (c) measuring the amount of displacement of said peptide on said sodium channel subtype by said small molecule.

36. The method of claim 35, wherein said peptide is radiolabeled.

37. The method of claim 35, wherein said sodium channel subtype is a neuronal sodium channel subtype and said peptide is μ-conopeptide S3.2 comprising an amino acid sequence as set forth in SEQ ID NO:211 or SEQ ID NO:432.

38. The method of claim 37, wherein said peptide is radiolabeled.

39. A method for screening a small molecule library to identify a small molecule which is a selective blocking agent of a sodium channel subtype comprising (a) allowing a small molecule to bind to a sodium channel subtype, (b) adding a peptide of claim 1 and (c) measuring the amount of displacement of said small molecule on said sodium channel subtype by said small peptide.

40. The method of claim 39, wherein said sodium channel subtype is a neuronal sodium channel subtype and said peptide is μ-conopeptide S3.2 comprising an amino acid sequence as set forth in SEQ ID NO:211 or SEQ ID NO:432.

41. A method of identifying compounds that mimic the therapeutic activity of a μ-conotoxin, comprising the steps of: (a) conducting a biological assay on a test compound to

determine the therapeutic activity; and (b) comparing the results obtained from the biological assay of the test compound to the results obtained from the biological assay of a μ-conotoxin, wherein said μ-conotoxin is a peptide of claim 1.

42. The method of claim 41, wherein said μ-conotoxin is S3.2 comprising an amino acid set forth in SEQ ID NO:211 or SEQ IN NO:432.

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agagcgtatg caggacgact ttataactga gcatcatccc ctgtttgatc ctgtcaaacg 180

gtgttgcgag aggccatgca acataggatg cgtaccttgt tgttaatgac cagctttgtc 240

atcgcggcct catcaagcga ataagtaaaa cgattgcagt 280

<210> 2
<211> 67
<212> PRT
<213> Conus arentus

<400> 2
Met Met Ser Lys Leu Gly Val Phe Leu Thr Ile Cys Met Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro
20 25 30

Ala Glu Arg Met Gln Asp Asp Phe Ile Thr Glu His His Pro Leu Phe

35 40 45

Asp Pro Val Lys Arg Cys Cys Glu Arg Pro Cys Asn Ile Gly Cys Val
50 55 60

Pro Cys Cys
65

<210> 3
<211> 14
<212> PRT
<213> Conus arentus

<220>
<221> PEPTIDE
<222> (1)..(14)
<223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 5 an
d 12 is Pro or Hy

<400> 3
Cys Cys Xaa Arg Xaa Cys Asn Ile Gly Cys Val Xaa Cys Cys
1 5 10

<210> 4
<211> 244
<212> DNA
<213> Conus atlanticus

<400> 4
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttccactt 60

actgctcttc cgctggatga agatcaaccg gtacaccgac ctgcagagcg tatgcaggac 120

atttcatctg atcaacatct cttctttgat ctcatcaaac ggtgctgcga gttgccatgc 180

gggccaggct tttgcgtccc ttgttgctga catcaataac gtgttgatga ccaactttct 240

cgag 244

<210> 5
<211> 69
<212> PRT
<213> Conus atlanticus

<400> 5
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
1 5 10 15

Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Val His
20 25 30

Arg Pro Ala Glu Arg Met Gln Asp Ile Ser Ser Asp Gln His Leu Phe
35 40 45

Phe Asp Leu Ile Lys Arg Cys Cys Glu Leu Pro Cys Gly Pro Gly Phe
50 55 60

Cys Val Pro Cys Cys
65

<210> 6
<211> 15
<212> PRT
<213> Conus atlanticus

<220>
<221> PEPTIDE
<222> (1)..(15)
<223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 5, 8 and 13 is Pro or Hy

<400> 6
Cys Cys Xaa Leu Xaa Cys Gly Xaa Gly Phe Cys Val Xaa Cys Cys
1 5 10 15

<210> 7
<211> 310
<212> DNA
<213> Conus aurisiacus

<400> 7
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgttt 60

gcttctgttt ccccttactg ctcttccgat ggatggagat caatctgtag accgacctga 120

agagcgtatg caggacgaca tttcatctga gcagcatccc ttgtttaatc agaaaagaat 180

gtgttgcggc gaaggccgga aatgccccag ctatttcaga aacagtcaga tttgtcattg 240

ttgttaaatg acaacgtgtc gatgaccaac ttcgttatca cgactaatga ataagtaaaa 300

cgattgcagt 310

<210> 8
<211> 74
<212> PRT
<213> Conus aurisiacus

<400> 8
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Ser Val Asp Arg Pro
20 25 30

Glu Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln His Pro Leu Phe
35 40 45

Asn Gln Lys Arg Met Cys Cys Gly Glu Gly Arg Lys Cys Pro Ser Tyr
50 55 60

Phe Arg Asn Ser Gln Ile Cys His Cys Cys
65 70

<210> 9
<211> 22
<212> PRT
<213> Conus aurisiacus
<220>
<221> PEPTIDE
<222> (1)..(22)
<223> Xaa at residue 5 is Glu or gamma-carboxy Glu; Xaa at residue 10 i s Pro or Hyp; Xaa at residue 12 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 9
Met Cys Cys Gly Xaa Gly Arg Lys Cys Xaa Ser Xaa Phe Arg Asn Ser
1 5 10 15

Gln Ile Cys His Cys Cys

20

<210> 10
<211> 257
<212> DNA
<213> Conus aurisiacus

<400> 10
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtttgcttct gtttcccctt 60

actgctcttc cgatcgatgg agatcaatct gtagaccgac ctgcagagcg tatgcaggat 120

gacatttcat ctgagcagca tcgcttgttc aatcagaaaa gaaggtgctg ccggtggcca 180

tgcccccgac aaatcgacgg tgaatattgt ggctgttgcc ttggatgata accgtgttga 240

tgaccaactt tctcgag 257

<210> 11
<211> 75
<212> PRT
<213> Conus aurisiacus

<400> 11
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
1 5 10 15

Leu Phe Pro Leu Thr Ala Leu Pro Ile Asp Gly Asp Gln Ser Val Asp
20 25 30

Arg Pro Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln His Arg
35 40 45

Leu Phe Asn Gln Lys Arg Arg Cys Cys Arg Trp Pro Cys Pro Arg Gln
50 55 60

Ile Asp Gly Glu Tyr Cys Gly Cys Cys Leu Gly
65 70 75

<210> 12
<211> 19
<212> PRT
<213> Conus aurisiacus

<220>
<221> PEPTIDE
<222> (1)..(19)
<223> Xaa at residue 13 is Glu or gamma-carboxy Glu; Xaa at residue 3 a nd 7 is Pro or Hyp; Xaa at residue4 is Trp or Bromo Trp; Xaa at residue 14 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho -Tyr or O-phospho-Ty

<400> 12
Cys Cys Arg Xaa Xaa Cys Xaa Arg Gln Ile Asp Gly Xaa Xaa Cys Gly
1 5 10 15

Cys Cys Leu

<210> 13
<211> 262
<212> DNA
<213> Conus aurisiacus

<400> 13
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctacttct gtttcccctt 60

actgcttttc cgatggatgg agatcaacct gcagaccaac ctgcagatcg tatgcaggac 120

gacatttcat ctgagcagta tcccttgttt gataagagac aaaagtgttg cactgggaag 180

aaggggtcat gctccggcaa agcatgcaaa aatctcaaat gttgctctgg acgataacgt 240

gttgatgacc aactttctcg ag 262

<210> 14
<211> 78
<212> PRT
<213> Conus aurisiacus

<400> 14
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
1 5 10 15

Leu Phe Pro Leu Thr Ala Phe Pro Met Asp Gly Asp Gln Pro Ala Asp
20 25 30

Gln Pro Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro
35 40 45

Leu Phe Asp Lys Arg Gln Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys
50 55 60

Ser Gly Lys Ala Cys Lys Asn Leu Lys Cys Cys Ser Gly Arg
65 70 75

<210> 15
<211> 23
<212> PRT
<213> Conus aurisiacus

<220>
<221> PEPTIDE
<222> (1)..(23)
<223> Xaa at residue 1 is Gln or pyro-Glu

<400> 15
Xaa Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys Ala Cys
1 5 10 15

Lys Asn Leu Lys Cys Cys Ser
20

<210> 16
<211> 232
<212> DNA
<213> Conus aurisiacus

<400> 16
ggatccatga tgtctaaact gggagtcttg ctgaccatct gtctgcttct gtttccactt 60

actgctgttc cgctggatgg agatcaacct ctagaccgac acgcggagcg tatgcatgat 120

ggcatttcac ctaaacgcca tccctggttt gatcccgtca aacggtgttg caaggtgcaa 180

tgcgagtctt gcacccсttg ttgctaacgt gttgatgacc aactttctcg ag 232

<210> 17
<211> 68
<212> PRT
<213> Conus aurisiacus

<400> 17
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
1 5 10 15

Leu Phe Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Leu Asp
20 25 30

Arg His Ala Glu Arg Met His Asp Gly Ile Ser Pro Lys Arg His Pro
35 40 45

Trp Phe Asp Pro Val Lys Arg Cys Cys Lys Val Gln Cys Glu Ser Cys
50 55 60

Thr Pro Cys Cys
65

<210> 18
<211> 13
<212> PRT
<213> Conus aurisiacus

<220>
<221> PEPTIDE
<222> (1)..(13)
<223> Xaa at residue 7 is Glu or gamma-carboxy Glu; Xaa at residue 11 i
s Pro or Hyp

<400> 18
Cys Cys Lys Val Gln Cys Xaa Ser Cys Thr Xaa Cys Cys
1 5 10

<210> 19
<211> 241
<212> DNA
<213> Conus bandus

<400> 19
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtatgcttct gtttcccctc 60

actgctcttc cgatggatgg agatcaacct gcagaccgac ctgcagagcg tagtcaggac 120
gtttcatctg aacagcatcc cttgtttgat cccgtcaaac ggtgttgcaa ctggccatgc 180

tccatgggat gcatcccttg ttgctactat taataacgtg ttgatgacca actttctcga 240

g 241

<210> 20
<211> 70
<212> PRT
<213> Conus bandus

<400> 20
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Met Leu
1 5 10 15

Leu Phe Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp
20 25 30

Arg Pro Ala Glu Arg Ser Gln Asp Val Ser Ser Glu Gln His Pro Leu
35 40 45

Phe Asp Pro Val Lys Arg Cys Cys Asn Trp Pro Cys Ser Met Gly Cys
50 55 60

Ile Pro Cys Cys Tyr Tyr
65 70

<210> 21
<211> 16
<212> PRT
<213> Conus bandus

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 5 and 12 is Pro or Hyp; Xaa at residue 4 is Trp or bromo-Trp; Xaa at residue 15 and 16 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 21
Cys Cys Asn Xaa Xaa Cys Ser Met Gly Cys Ile Xaa Cys Cys Xaa Xaa
1 5 10 15

<210> 22
<211> 298
<212> DNA
<213> Conus betulinus

<400> 22
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccttctgtct 60

gcttctgttt cccctgactg ctcttccgct ggatgaagat caacctgcag accgacctgc 120

agagcgtatg caggacattt catctgaaca gcatcccttg tttgatcccg tcaaacggtg 180

ttgcgaattg ccatgccatg gatgcgtccc ttgttgctgg ccttaataac gtgtggatga 240

ccaactgtgt tatcacggcc acgtcaagtg tctaatgaat aagtaaaatg attgcagt 298

<210> 23
<211> 67
<212> PRT
<213> Conus betulinus

<400> 23
Met Met Ser Lys Leu Gly Val Leu Leu Thr Phe Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Ala Asp Arg Pro
20 25 30

Ala Glu Arg Met Gln Asp Ile Ser Ser Glu Gln His Pro Leu Phe Asp
35 40 45

Pro Val Lys Arg Cys Cys Glu Leu Pro Cys His Gly Cys Val Pro Cys
50 55 60

Cys Trp Pro
65

<210> 24
<211> 15
<212> PRT
<213> Conus betulinus

<220>
<221> PEPTIDE
<222> (1)..(15)
<223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 5, 1

1 and 15 is Pro or Hyp; Xaa at residue 14 is Trp or bromo-Trp

<400> 24
Cys Cys Xaa Leu Xaa Cys His Gly Cys Val Xaa Cys Cys Xaa Xaa
1 5 10 15

<210> 25
<211> 298
<212> DNA
<213> Conus betulinus

<400> 25
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccttctgtct 60

gcttctgttt cccctgactg ctcttcc__t ggatgaagat caacctgcag accgacatgc 120

agagcgtatg caggacattt cacctgaaca gcatccctcg tttgatcccg tcaaacggtg 180

ttgcgggctg ccatgcaatg gatgcgtccc ttgttgctgg ccttcataac gtgtggacga 240

ccaactttgt tatcacggcc acgtcaagtg tctgatgaat aagtaaaacg attgcagt 298

<210> 26
<211> 68
<212> PRT
<213> Conus betulinus

<400> 26
Met Met Ser Lys Leu Gly Val Leu Leu Thr Phe Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Ala Asp Arg His
20 25 30
Ala Glu Arg Met Gln Asp Ile Ser Pro Glu Gln His Pro Ser Phe Asp
35 40 45

Pro Val Lys Arg Cys Cys Gly Leu Pro Cys Asn Gly Cys Val Pro Cys
50 55 60

Cys Trp Pro Ser
65

<210> 27
<211> 16
<212> PRT
<213> Conus betulinus

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 5, 11 and 15 is Pro or Hyp; Xaa at residue 14 is T
rp or bromo-Tr

<400> 27
Cys Cys Gly Leu Xaa Cys Asn Gly Cys Val Xaa Cys Cys Xaa Xaa Ser
1 5 10 15

<210> 28
<211> 282
<212> DNA
<213> Conus betulinus

<400> 28
caagagggat cgatagcagt tcatgatgtt taaactggga gtcttgttga ccatctatat 60

gcttctgttt ccctttactg ctcttccgct ggatggagat caacctgcag accaacctct 120

agagcgcatg cagtatgaca tgttacgtgc agtgaatccc tggtttgatc ccgtcaaaag 180

gtgctgctcg aggaactgcg cagtatgcat cccttgttgc ccgaattggc cagcttgatt 240

atcgcggcca agagtctaat gaataagtaa aacgattgca gt 282

<210> 29
<211> 71
<212> PRT
<213> Conus betulinus

<400> 29
Met Met Phe Lys Leu Gly Val Leu Leu Thr Ile Tyr Met Leu Leu Phe
1 5 10 15

Pro Phe Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Pro
20 25 30

Leu Glu Arg Met Gln Tyr Asp Met Leu Arg Ala Val Asn Pro Trp Phe
35 40 45

Asp Pro Val Lys Arg Cys Cys Ser Arg Asn Cys Ala Val Cys Ile Pro
50 55 60

Cys Cys Pro Asn Trp Pro Ala
65 70

<210> 30
<211> 18
<212> PRT
<213> Conus betulinus

<220>
<221> PEPTIDE
<222> (1)..(18)
<223> Xaa at residue 11, 14 and 17 is Pro or Hyp; Xaa at residue 16 is
Trp or bromo-Tr

<400> 30
Cys Cys Ser Arg Asn Cys Ala Val Cys Ile Xaa Cys Cys Xaa Asn Xaa
1 5 10 15

Xaa Ala

<210> 31
<211> 325
<212> DNA
<213> Conus bullatus

<400> 31
caagaaggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct 60

gcttctgttt cccctttttg ctcttccgca ggatggagat caacctgcag accgacctgc 120

agagcgtatg caggacgaca tttcatctga gcagaattcc ttgcttgaga agagagttac 180

tgacaggtgc tgcaaaggga agagggaatg cggcagatgg tgcagagatc actcgcgttg 240

ttgcggtcga cgataagctg ttgatgacca gctttgttat cacggctaca tcaagtgtct 300

agtgaataag taaaatgatt gcagt 325

<210> 32

<211> 77
<212> PRT
<213> Conus bullatus

<400> 32
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Phe Ala Leu Pro Gln Asp Gly Asp Gln Pro Ala Asp Arg Pro
20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Asn Ser Leu Leu
35 40 45

Glu Lys Arg Val Thr Asp Arg Cys Cys Lys Gly Lys Arg Glu Cys Gly
50 55 60

Arg Trp Cys Arg Asp His Ser Arg Cys Cys Gly Arg Arg
65 70 75

<210> 33
<211> 23
<212> PRT
<213> Conus bullatus

<220>
<221> PEPTIDE
<222> (1)..(23)
<223> Xaa at residue 11 is Glu or gamma-carboxy Glu; Xaa at residue 15 is Trp or bromo-Tr

<400> 33
Val Thr Asp Arg Cys Cys Lys Gly Lys Arg Xaa Cys Gly Arg Xaa Cys
1 5 10 15

Arg Asp His Ser Arg Cys Cys
20

<210> 34
<211> 326
<212> DNA
<213> Conus bullatus

<400> 34
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct 60

gcttctgttt cccctttttg ctcttcggca ggatggagat caacctgcag accgacctgc 120

agagcgtatg caggatgaca tttcatctga gcagaatccc ttgcttgaga agagagttgg 180

tgacaggtgc tgcaaaggga agagggggtg cggcagatgg tgcagagatc actcacgttg 240

ttgcggtcga cgataacgtg ttgatgacca gctttgttat cacggctaca tcaagtgtct 300

tagtgattaa gtaaaacgat tgcagt 326

<210> 35
<211> 77
<212> PRT
<213> Conus bullatus

<400> 35
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

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Pro Leu Phe Ala Leu Arg Gln Asp Gly Asp Gln Pro Ala Asp Arg Pro
            20                  25                  30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Asn Pro Leu Leu
        35                  40                  45

Glu Lys Arg Val Gly Asp Arg Cys Cys Lys Gly Lys Arg Gly Cys Gly
    50                  55                  60

Arg Trp Cys Arg Asp His Ser Arg Cys Cys Gly Arg Arg
65                  70                  75

<210>  36
<211>  23
<212>  PRT
<213>  Conus bullatus

<220>
<221>  PEPTIDE
<222>  (1)..(23)
<223>  Xaa at residue 15 is Trp or bromo-Trp
<400>  36
Val Gly Asp Arg Cys Cys Lys Gly Lys Arg Gly Cys Gly Arg Xaa Cys
1               5                   10                  15

Arg Asp His Ser Arg Cys Cys
            20

<210>  37
<211>  331
<212>  DNA
<213>  Conus bullatus

<400>  37
caagaaggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct      60

gcttctgttt cccctttttg ctcttccgca ggatggagat caacctgcag accgacctgc     120

agagcgtatg caggacgaca tttcatctga gcagaatccc ttgcttgaga agagagttgg     180

tgaaaggtgc tgcaaaaacg ggaagagggg gtgcggcaga tggtgcagag atcactcacg     240

ttgttgcggt cgacgataac gtgttgatga ccgaggcttt cgttatcacg gctacatcaa     300

gtgtctagtg aataagtaaa acgattgcag t                                    331

<210>  38
<211>  78
<212>  PRT
<213>  Conus bullatus

<400>  38
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1               5                   10                  15

Pro Leu Phe Ala Leu Pro Gln Asp Gly Asp Gln Pro Ala Asp Arg Pro
            20                  25                  30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Asn Pro Leu Leu
        35                  40                  45

Glu Lys Arg Val Gly Glu Arg Cys Cys Lys Asn Gly Lys Arg Gly Cys
    50                  55                  60

Gly Arg Trp Cys Arg Asp His Ser Arg Cys Cys Gly Arg Arg
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65 70 75

<210> 39
<211> 24
<212> PRT
<213> Conus bullatus

<220>
<221> PEPTIDE
<222> (1)..(24)
<223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 16 i
s Trp or bromo-Tr

<400> 39
Val Gly Xaa Arg Cys Cys Lys Asn Gly Lys Arg Gly Cys Gly Arg Xaa
1 5 10 15

Cys Arg Asp His Ser Arg Cys Cys
20

<210> 40
<211> 337
<212> DNA
<213> Conus bullatus

<400> 40
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct 60

gcttctgttt cccctttttg ctcttccgca ggacggagat caacctgcag accgacctgc 120

agagcgtatg caggacgacc tttcatctga gcagcatccc ttgtttgaga agagaattgt 180

tgacaggtgc tgcaacaaag ggaacgggaa gaggggtgc agcagatggt gcagagatca 240

ctcacgttgt tgcggtcgac gatgaactgt tgatgaccga ggctttggtt atcacggcta 300

catcaagtgt ctagtgaata agtaaaacga ttgcagt 337

<210> 41
<211> 80
<212> PRT
<213> Conus bullatus

<400> 41
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Phe Ala Leu Pro Gln Asp Gly Asp Gln Pro Ala Asp Arg Pro
20 25 30

Ala Glu Arg Met Gln Asp Asp Leu Ser Ser Glu Gln His Pro Leu Phe
35 40 45

Glu Lys Arg Ile Val Asp Arg Cys Cys Asn Lys Gly Asn Gly Lys Arg
50 55 60

Gly Cys Ser Arg Trp Cys Arg Asp His Ser Arg Cys Cys Gly Arg Arg
65 70 75 80

<210> 42
<211> 26
<212> PRT
<213> Conus bullatus

<220>

<221> PEPTIDE
<222> (1)..(26)
<223> Xaa at residue 18 is Trp or bromo-Trp

<400> 42
Ile Val Asp Arg Cys Cys Asn Lys Gly Asn Gly Lys Arg Gly Cys Ser
1 5 10 15

Arg Xaa Cys Arg Asp His Ser Arg Cys Cys
20 25

<210> 43
<211> 337
<212> DNA
<213> Conus bullatus

<400> 43
caagaaggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct 60

gcttctgttt ccccttttg ctcttccgca ggatggagat caacctgcag accgacctgc 120

tgagcgtatg caggacgaca tttcatctga gcggaatccc ttgtttgaga agagcgttgg 180

tttatattgc tgccgaccca aacccaacgg gcagatgatg tgcgacagat ggtgcgaaaa 240

aaactcacgt tgttgcggtc gacgataatg tgttgatgac cagctttgtt atcaaggcta 300

catcaagtat ctagtgaata agtaaaacga ttgcagt 337

<210> 44
<211> 77
<212> PRT
<213> Conus bullatus

<400> 44
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Phe Ala Leu Pro Gln Asp Gly Asp Gln Pro Ala Asp Arg Pro
20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Asn Pro Leu Phe Glu Lys
35 40 45

Ser Val Gly Cys Cys Arg Pro Lys Pro Asn Gly Gln Met Met Cys Asp
50 55 60

Arg Trp Cys Glu Lys Asn Ser Arg Cys Cys Gly Arg Arg
65 70 75

<210> 45
<211> 27
<212> PRT
<213> Conus bullatus

<220>
<221> PEPTIDE
<222> (1)..(27)
<223> Xaa at residue 21 is Glu or gamma-carboxy Glu; Xaa at residue 8 a
nd 10 is Pro or Hyp; Xaa at residue 19 is Trp or bromo-Trp; Xaa a
t residue 4 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulph
o-Tyr or O-phospho-Ty

<400> 45
Val Gly Leu Xaa Cys Cys Arg Xaa Lys Xaa Asn Gly Gln Met Met Cys

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1               5                   10                  15

Asp Arg Xaa Cys Xaa Lys Asn Ser Arg Cys Cys
            20                  25
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<210> 46
<211> 323
<212> DNA
<213> Conus bullatus
<400> 46

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caagaaggat cgatagcagt tcatgatgtc taaactggga gttttgttga ccatctgtct    60

gcttctgttt ccccttactg ctcttccgat ggatggagat caatctgtag accgacctgc   120

agaacgtatg caggacgacc tttcatctga gcagcatccc ttgtttgttc agaaaagaag   180

gtgttgcggc gaaggcttga catgccccag atattggaaa aacagtcaga tttgtgcttg   240

ttgttaaatg acaacgtgtc gatgaccaac ttcggtatca cgactacgcc aagtgtctaa   300

tgaataagta aaacgattgc agt                                           323
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<210> 47
<211> 74
<212> PRT
<213> Conus bullatus

<400> 47

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Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1               5                   10                  15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Ser Val Asp Arg Pro
            20                  25                  30

Ala Glu Arg Met Gln Asp Asp Leu Ser Ser Glu Gln His Pro Leu Phe
        35                  40                  45

Val Gln Lys Arg Arg Cys Cys Gly Glu Gly Leu Thr Cys Pro Arg Tyr
    50                  55                  60

Trp Lys Asn Ser Gln Ile Cys Ala Cys Cys
65                  70
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<210> 48
<211> 22
<212> PRT
<213> Conus bullatus

<220>
<221> PEPTIDE
<222> (1)..(22)
<223> Xaa at residue 5 is Glu or gamma-carboxy Glu; Xaa at residue 10 i
s Pro or Hyp; Xaa at residue 13 is Trp or bromo-Trp; Xaa at resid
ue 12 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
or O-phospho-Ty

<400> 48

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Arg Cys Cys Gly Xaa Gly Leu Thr Cys Xaa Arg Xaa Xaa Lys Asn Ser
1               5                   10                  15

Gln Ile Cys Ala Cys Cys
            20
```

<210> 49
<211> 322

<212> DNA
<213> Conus bullatus

<400> 49
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct 60
gcttctgttt ccccttttg ctcttccgca ggatggagat caacctgcag accgacctgc 120

tgagcgtatg caggacgaca tttcatctga gcaggatccc ttgtttgttc agaaaagaag 180

gtgttgcggc gaaggcttga catgccccag atattggaaa aacagtcaga tttgtgcttg 240

ttgttaaatg acaacgtgtg atgaccaact tcggtatcac gactacgcca agtgtctaat 300

gaataagtaa aacgattgca gt 322

<210> 50
<211> 74
<212> PRT
<213> Conus bullatus

<400> 50
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Phe Ala Leu Pro Gln Asp Gly Asp Gln Pro Ala Asp Arg Pro
20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Asp Pro Leu Phe
35 40 45

Val Gln Lys Arg Arg Cys Cys Gly Glu Gly Leu Thr Cys Pro Arg Tyr
50 55 60

Trp Lys Asn Ser Gln Ile Cys Ala Cys Cys
65 70

<210> 51
<211> 22
<212> PRT
<213> Conus bullatus

<220>
<221> PEPTIDE
<222> (1)..(22)
<223> Xaa at residue 5 is Glu or gamma-carboxy Glu; Xaa at residue 10 i
s Pro or Hyp; Xaa at residue 13 is Trp or bromo-Trp; Xaa at resid
ue 12 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
or O-phospho-Ty

<400> 51
Arg Cys Cys Gly Xaa Gly Leu Thr Cys Xaa Arg Xaa Xaa Lys Asn Ser
1 5 10 15

Gln Ile Cys Ala Cys Cys
20

<210> 52
<211> 238
<212> DNA
<213> Conus capitaneus

<400> 52
ggatccatga tgtctaaact gggagtcttg gtgaccatct gcctgcttct gtttcccctt 60

gctgcttttc cactggatgg aaatcaacct gcagaccacc ctgcaaagcg tacgcaagat 120

gacagttcag ctgccctgat caatacctgg attgatcatt cccattcttg ctgcagggac 180

tgcggtgaag attgtgttgg ttgttgccgg taacgtgttg atgaccaact ttctcgag 238

<210> 53
<211> 70
<212> PRT
<213> Conus capitaneus

<400> 53
Gly Ser Met Met Ser Lys Leu Gly Val Leu Val Thr Ile Cys Leu Leu
1 5 10 15

Leu Phe Pro Leu Ala Ala Phe Pro Leu Asp Gly Asn Gln Pro Ala Asp
20 25 30

His Pro Ala Lys Arg Thr Gln Asp Asp Ser Ser Ala Ala Leu Ile Asn
35 40 45

Thr Trp Ile Asp His Ser His Ser Cys Cys Arg Asp Cys Gly Glu Asp
50 55 60

Cys Val Gly Cys Cys Arg
65 70

<210> 54
<211> 15
<212> PRT
<213> Conus capitaneus

<220>
<221> PEPTIDE
<222> (1)..(15)
<223> Xaa at residue 8 is Glu or gamma-carboxy Glu

<400> 54
Ser Cys Cys Arg Asp Cys Gly Xaa Asp Cys Val Gly Cys Cys Arg
1 5 10 15

<210> 55
<211> 323
<212> DNA
<213> Conus caracteristicus

<400> 55
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct 60

gcttctgttt ccccttactg ctcttccaat ggatggagat caacctgcag accaacctgc 120

agatcgtatg caggacgaca tttcatctga gcagtatccc ttgtttgata tgagaaaaag 180

gtgttgcggc cccggcggtt catgccccgt atatttcaga gacaatttta tttgtggttg 240

ttgttaaatg acaacgtgtc gatgaccaac ttcattatca cgactacgcc aagtgtctaa 300

tgaataagta aaatgattgc agt 323

<210> 56
<211> 74
<212> PRT
<213> Conus caracteristicus

<400> 56

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro
20 25 30

Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe
35 40 45

Asp Met Arg Lys Arg Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr
50 55 60

Phe Arg Asp Asn Phe Ile Cys Gly Cys Cys
65 70

<210> 57
<211> 21
<212> PRT
<213> Conus caracteristicus

<220>
<221> PEPTIDE
<222> (1)..(21)
<223> Xaa at residue 4 and 9 is Pro or Hyp; Xaa at residue 11 is Tyr, 1
25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 57
Cys Cys Gly Xaa Gly Gly Ser Cys Xaa Val Xaa Phe Arg Asp Asn Phe
1 5 10 15

Ile Cys Gly Cys Cys
20

<210> 58
<211> 316
<212> DNA
<213> Conus caracteristicus

<400> 58
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct 60

gcttctgttt ccccttactg ctcttccgat ggatggagat gaacctgcaa accgacctgt 120

cgagcgtatg caggacaaca tttcatctga gcagtatccc ttgtttgaga agagacgaga 180

ttgttgcact ccgccgaaga aatgcaaaga ccgacaatgc aaaccccaga gatgttgcgc 240

tggacgataa cgtgttgatg accaacttta tcacggctac gtcaagtgtt tagtgaataa 300

gtaaaatgat tgcagt 316

<210> 59
<211> 75
<212> PRT
<213> Conus caracteristicus

<400> 59
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Glu Pro Ala Asn Arg Pro
20 25 30

Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln Tyr Pro Leu Phe

35 40 45

Glu Lys Arg Arg Asp Cys Cys Thr Pro Pro Lys Lys Cys Lys Asp Arg
50 55 60

Gln Cys Lys Pro Gln Arg Cys Cys Ala Gly Arg
65 70 75

<210> 60
<211> 22
<212> PRT
<213> Conus caracteristicus

<220>
<221> PEPTIDE
<222> (1)..(22)
<223> Xaa at residue 6, 7 and 17 is Pro or Hyp

<400> 60
Arg Asp Cys Cys Thr Xaa Xaa Lys Lys Cys Lys Asp Arg Gln Cys Lys
1 5 10 15

Xaa Gln Arg Cys Cys Ala
20

<210> 61
<211> 314
<212> DNA
<213> Conus caracteristicus

<400> 61
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct 60

gcttctgttt ccccttactg ctcttccact ggatggagat caacctgcag atcaatctgc 120

agagcgacct gcagagcgta cgcaggacga cattcagcag catccgttat atgatccgaa 180

aagaaggtgt tgccgttatc catgccccga cagctgccac ggatcttgct gctataagtg 240

ataacatgtt gatggccagc tttgttatca cggccacgtc aagtgtctta atgaataagt 300

aaaacgattg cagt 314

<210> 62
<211> 72
<212> PRT
<213> Conus caracteristicus

<400> 62
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Ser
20 25 30
Ala Glu Arg Pro Ala Glu Arg Thr Gln Asp Asp Ile Gln Gln His Pro
35 40 45

Leu Tyr Asp Pro Lys Arg Arg Cys Cys Arg Tyr Pro Cys Pro Asp Ser
50 55 60

Cys His Gly Ser Cys Cys Tyr Lys
65 70

<210> 63
<211> 18

<212> PRT
<213> Conus caracteristicus

<220>
<221> PEPTIDE
<222> (1)..(18)
<223> Xaa at residue 6 and 8 is Pro or Hyp; Xaa at residue 5 and 17 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phos pho-Ty

<400> 63
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Arg Cys Cys Arg Xaa Xaa Cys Xaa Asp Ser Cys His Gly Ser Cys Cys
1               5                   10                  15

Xaa Lys
```

<210> 64
<211> 292
<212> DNA
<213> Conus caracteristicus

<400> 64
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caagagggat cgatagcagt tcatgatgtc taaactggga gccttgttga ccatctgtct      60

acttctgttt tcccttactg ctgttccgct ggatggagat caacatgcag accaacctgc     120

acagcgtctg caggaccgca ttccaactga agatcatccc ttatttgatc ccaacaaacg     180

gtgttgcccg ccggtggcat gcaacatggg atgcaagcct tgttgtggat gaccagcttt     240

gttatcgcgg tcttcatgaa gtgtcttaat gaataagtaa aatgattgca gt             292
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<210> 65
<211> 69
<212> PRT
<213> Conus caracteristicus

<400> 65
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Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe
1               5                   10                  15

Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
            20                  25                  30

Ala Gln Arg Leu Gln Asp Arg Ile Pro Thr Glu Asp His Pro Leu Phe
        35                  40                  45

Asp Pro Asn Lys Arg Cys Cys Pro Pro Val Ala Cys Asn Met Gly Cys
    50                  55                  60

Lys Pro Cys Cys Gly
65
```

<210> 66
<211> 15
<212> PRT
<213> Conus caracteristicus

<220>
<221> PEPTIDE
<222> (1)..(15)
<223> Xaa at residue 3, 4 and 13 is Pro or Hyp

<400> 66
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Cys Cys Xaa Xaa Val Ala Cys Asn Met Gly Cys Lys Xaa Cys Cys
```

1 5 10 15

<210> 67
<211> 293
<212> DNA
<213> Conus caracteristicus

<400> 67
caagagggat cgatagcagt tcatgatgtc taaactggga gccttgttga ccatctgtct 60

acttctgttt tccctaactg ctgttccgct ggatggagat caacatgcag accaacctgc 120

agagcgtctg catgaccgcc ttccaactga aaatcatccc ttatatgatc ccgtcaaacg 180

gtgttgcgat gattcggaat gcgactattc ttgctggcct tgctgtatgt ttggataacc 240

tttgttatcg cggcctcatc aagtgtctaa tgaataagta aaacgattgc agt 293

<210> 68
<211> 71
<212> PRT
<213> Conus caracteristicus

<400> 68
Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
20 25 30

Ala Glu Arg Leu His Asp Arg Leu Pro Thr Glu Asn His Pro Leu Tyr
35 40 45

Asp Pro Val Lys Arg Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys
50 55 60

Trp Pro Cys Cys Met Phe Gly
65 70

<210> 69
<211> 17
<212> PRT
<213> Conus caracteristicus

<220>
<221> PEPTIDE
<222> (1)..(17)
<223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 i
s Pro or Hyp; Xaa at residue 12 is Trp or bromo-Trp; Xaa at resid
ue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr o
r O-phospho-Ty

<400> 69
Cys Cys Asp Asp Ser Xaa Cys Asp Xaa Ser Cys Xaa Xaa Cys Cys Met
1 5 10 15

Phe

<210> 70
<211> 232
<212> DNA
<213> Conus caracteristicus

<400> 70
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt 60

actgctgttc cgctggatgg agatcaacct gcagaccgac ctgcagagcg taagcaggac 120

gtttcatctg aacagcatcc cttctttgat cccgtcaaac ggtgttgccg ccggtgttac 180

atgggatgca tcccttgttg cttttaacgt gttgatgacc aactttctcg ag 232

<210> 71
<211> 68
<212> PRT
<213> Conus caracteristicus

<400> 71
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
1 5 10 15

Leu Phe Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp
20 25 30

Arg Pro Ala Glu Arg Lys Gln Asp Val Ser Ser Glu Gln His Pro Phe
35 40 45

Phe Asp Pro Val Lys Arg Cys Cys Arg Arg Cys Tyr Met Gly Cys Ile
50 55 60

Pro Cys Cys Phe
65

<210> 72
<211> 14
<212> PRT
<213> Conus caracteristicus

<220>
<221> PEPTIDE
<222> (1)..(14)
<223> Xaa at residue 11 is Pro or Hyp; Xaa at residue 6 is Tyr, 125I-Ty
r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 72
Cys Cys Arg Arg Cys Xaa Met Gly Cys Ile Xaa Cys Cys Phe
1 5 10
<210> 73
<211> 323
<212> DNA
<213> Conus circumcisus

<400> 73
caagaaggat cgatagcagt tcatgatgtc taaactgggg gtattgttga ccatctgtct 60

gcttctgttt ccccttactg ctcttccaat ggatggagat caacctgcag accaacctgc 120

agatcgtatg caggacgaca tttcatctga gcagtatccc ttgtttgata agagacgaaa 180

gtgttgcggc aaagacgggc catgccccaa atatttcaaa gacaatttta tttgtggttg 240

ttgttaaatg acaacgtgtc gatgaccaac ttcgttatca cgattcgcca agtgtcttaa 300

tgaataagta aaatgattgc agt 323

<210> 74
<211> 74
<212> PRT
<213> Conus circumcisus

<400> 74
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro
20 25 30

Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe
35 40 45

Asp Lys Arg Arg Lys Cys Cys Gly Lys Asp Gly Pro Cys Pro Lys Tyr
50 55 60

Phe Lys Asp Asn Phe Ile Cys Gly Cys Cys
65 70

<210> 75
<211> 23
<212> PRT
<213> Conus circumcisus

<220>
<221> PEPTIDE
<222> (1)..(23)
<223> Xaa at residue 9 and 11 is Pro or Hyp; Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-T y

<400> 75
Arg Lys Cys Cys Gly Lys Asp Gly Xaa Cys Xaa Lys Xaa Phe Lys Asp
1 5 10 15

Asn Phe Ile Cys Gly Cys Cys
20

<210> 76
<211> 293
<212> DNA
<213> Conus dalli

<400> 76
caagagggat cgatagcagt tcatgatgtc taaactggga gccttgttga ccatctgtct 60

acttctgttt tccctaactg ctgttccgct ggatggagat caacatgcag accaacctgc 120

agagcgtctg caggaccgcc ttccaactga aaatcatccc ttatatgatc ccgtcaaacg 180

gtgttgcgat gattcggaat gcgactattc ttgctggcct tgctgtattt tatcataacc 240

tttgttatcg cggcctcatc aagtgtcaaa tgaataagta aaatgattgc agt 293

<210> 77
<211> 71
<212> PRT
<213> Conus dalli

<400> 77
Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
20 25 30

Ala Glu Arg Leu Gln Asp Arg Leu Pro Thr Glu Asn His Pro Leu Tyr
35 40 45

```
Asp Pro Val Lys Arg Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys
    50                  55                  60

Trp Pro Cys Cys Ile Leu Ser
65                  70
```

<210> 78
<211> 18
<212> PRT
<213> Conus dalli

<220>
<221> PEPTIDE
<222> (1)..(18)
<223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 is Pro or Hyp; Xaa at residue 12 is Trp or bromo-Trp; Xaa at residue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 78

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Cys Cys Asp Asp Ser Xaa Cys Asp Xaa Ser Cys Xaa Xaa Cys Cys Ile
1               5                   10                  15

Leu Ser
```

<210> 79
<211> 299
<212> DNA
<213> Conus dalli

<400> 79

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caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatttgtct      60

acttctgttt ccccttactg ctgttccact ggatggagat cagcctgcag accgacctgc     120

agagcgtatg caggacggca tttcatctga acatcatcca ttttttgatt ccgtcaaaaa     180

gaaacaacag tgttgcccgc cggtggcatg caacatggga tgcgagcctt gttgtggatg     240

accagctttg ttatcgcggc tcatgaagtg tcctaatgaa taagtaaaac gattgcagt      299
```

<210> 80
<211> 72
<212> PRT
<213> Conus dalli

<400> 80

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Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1               5                   10                  15

Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro
            20                  25                  30

Ala Glu Arg Met Gln Asp Gly Ile Ser Ser Glu His His Pro Phe Phe
        35                  40                  45

Asp Ser Val Lys Lys Lys Gln Gln Cys Cys Pro Pro Val Ala Cys Asn
    50                  55                  60

Met Gly Cys Glu Pro Cys Cys Gly
65                  70
```

<210> 81
<211> 17

<212> PRT
<213> Conus dalli

<220>
<221> PEPTIDE
<222> (1)..(17)
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 14 is Glu or gamma-carboxy Glu; Xaa at residue 5, 6 and 15is Pro or Hyp

<400> 81
Xaa Gln Cys Cys Xaa Xaa Val Ala Cys Asn Met Gly Cys Xaa Xaa Cys
1 5 10 15

Cys

<210> 82
<211> 290
<212> DNA
<213> Conus dalli

<400> 82
caagaaggat cgatagcagt tcatgatgtc taaactggga gtcttgttga tcatatgtct 60

atttctgttt ccccttactg ctgttcagct caatggagat cagcctgcag accaatctgc 120

agagcgtatg caggacaaaa tttcatctga acatcatccc ttttttgatc ccgtcaaacg 180

ttgttgcaac gcggggtttt gccgcttcgg atgcacgcct tgttgttggt gaccagcttt 240

gttatcgcgg cctcatcaag tgtctaatga ataagtaaaa tgattgcagt 290
<210> 83
<211> 69
<212> PRT
<213> Conus dalli

<400> 83
Met Met Ser Lys Leu Gly Val Leu Leu Ile Ile Cys Leu Phe Leu Phe
1 5 10 15

Pro Leu Thr Ala Val Gln Leu Asn Gly Asp Gln Pro Ala Asp Gln Ser
20 25 30

Ala Glu Arg Met Gln Asp Lys Ile Ser Ser Glu His His Pro Phe Phe
35 40 45

Asp Pro Val Lys Arg Cys Cys Asn Ala Gly Phe Cys Arg Phe Gly Cys
50 55 60

Thr Pro Cys Cys Trp
65

<210> 84
<211> 16
<212> PRT
<213> Conus dalli

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 13 is Pro or Hyp; Xaa at residue 16 is Trp or brom o-Tr

<400> 84
Cys Cys Asn Ala Gly Phe Cys Arg Phe Gly Cys Thr Xaa Cys Cys Xaa
1 5 10 15

<210> 85
<211> 288
<212> DNA
<213> Conus distans

<400> 85
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgctga ccatctttct 60

gcttctgttt ccccttactg ctgttccgct ggatggagat caacccgcag acggacttgc 120

agagcgcatg caggacgaca gttcagctgc actgattaga gactggcttc ttcaaacccg 180

acagtgttgt gtgcatccat gcccatgcac gccttgctgt agatgaccag ctttgtcatc 240

gcggctacgt caagtatcta atgaataagt aagtaaaacg attgcagt 288

<210> 86
<211> 67
<212> PRT
<213> Conus distans

<400> 86
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Phe Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Gly Leu
20 25 30

Ala Glu Arg Met Gln Asp Asp Ser Ser Ala Ala Leu Ile Arg Asp Trp
35 40 45

Leu Leu Gln Thr Arg Gln Cys Cys Val His Pro Cys Pro Cys Thr Pro
50 55 60

Cys Cys Arg
65

<210> 87
<211> 14
<212> PRT
<213> Conus distans

<220>
<221> PEPTIDE
<222> (1)..(14)
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6, 8 and 11 i
s Pro or Hy

<400> 87
Xaa Cys Cys Val His Xaa Cys Xaa Cys Thr Xaa Cys Cys Arg
1 5 10

<210> 88
<211> 303
<212> DNA
<213> Conus ermineus

<400> 88
acctcaagag ggatcgatcg cagttcatga tgtctaaact gggagccttg ttgaccatct 60

gtctgcttct gtttcccatt actgctcttc tgatggatgg agatcagcct gcagaccgac 120

ctgcagagcg tacggaggat gacatttcat ctgactacat tccctgttgc agttggccat 180

gcccccgata ctccaacggt aaacttgttt gtttttgttg ccttggatga taatgtgttg 240

atgaccaact ttgttatcac ggctacgtca agtgtctact gaataagtaa aatgattgca 300

gta 303

<210> 89
<211> 67
<212> PRT
<213> Conus ermineus

<400> 89
Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Ile Thr Ala Leu Leu Met Asp Gly Asp Gln Pro Ala Asp Arg Pro
20 25 30

Ala Glu Arg Thr Glu Asp Asp Ile Ser Ser Asp Tyr Ile Pro Cys Cys
35 40 45

Ser Trp Pro Cys Pro Arg Tyr Ser Asn Gly Lys Leu Val Cys Phe Cys
50 55 60

Cys Leu Gly
65

<210> 90
<211> 20
<212> PRT
<213> Conus ermineus

<220>
<221> PEPTIDE
<222> (1)..(20)
<223> Xaa at residue 5 and 7 is Pro or Hyp; Xaa at residue4 is Trp or bromo-Trp; Xaa at residue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-i odo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 90
Cys Cys Ser Xaa Xaa Cys Xaa Arg Xaa Ser Asn Gly Lys Leu Val Cys
1 5 10 15

Phe Cys Cys Leu
20

<210> 91
<211> 241
<212> DNA
<213> Conus generalis

<400> 91
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctggttct gtttcccctt 60

actgctcttc cactggatgg agaacaacct gtagaccgac atgccgagca tatgcaggat 120

gacaattcag ctgcacagaa cccctgggtt attgccatca gacagtgttg cacgttctgc 180

aactttggat gccaaccttg ttgcctcacc tgataacgtg ttgatgacca actttctcga 240

g 241

<210> 92
<211> 70
<212> PRT

<213> Conus generalis

<400> 92
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Val
1 5 10 15

Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Gly Glu Gln Pro Val Asp
20 25 30

Arg His Ala Glu His Met Gln Asp Asp Asn Ser Ala Ala Gln Asn Pro
35 40 45

Trp Val Ile Ala Ile Arg Gln Cys Cys Thr Phe Cys Asn Phe Gly Cys
50 55 60

Gln Pro Cys Cys Leu Thr
65 70

<210> 93
<211> 16
<212> PRT
<213> Conus generalis

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 12 is Pro or Hy

<400> 93
Xaa Cys Cys Thr Phe Cys Asn Phe Gly Cys Gln Xaa Cys Cys Leu Thr
1 5 10 15

<210> 94
<211> 241
<212> DNA
<213> Conus generalis

<400> 94
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctggttct gtttcccctt 60

actgctcttc cactggatgg agaacaacct gtagaccgac atgccgagca tatgcaggat 120

gacaattcag ctgcacagaa cccctgggtt attgccatca gacagtgttg cacgttctgc 180

aactttggat gccagccttg ttgcgtcccc tgataacgtg ttgatgacca actttctcga 240

g 241

<210> 95
<211> 70
<212> PRT
<213> Conus generalis

<400> 95
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Val
1 5 10 15

Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Gly Glu Gln Pro Val Asp
20 25 30

Arg His Ala Glu His Met Gln Asp Asp Asn Ser Ala Ala Gln Asn Pro
35 40 45

Trp Val Ile Ala Ile Arg Gln Cys Cys Thr Phe Cys Asn Phe Gly Cys

50 55 60

Gln Pro Cys Cys Val Pro
65 70

<210> 96
<211> 16
<212> PRT
<213> Conus generalis

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 12 and 16 is Pro or Hy

<400> 96
Xaa Cys Cys Thr Phe Cys Asn Phe Gly Cys Gln Xaa Cys Cys Val Xaa
1 5 10 15

<210> 97
<211> 862
<212> DNA
<213> Conus geographus

<400> 97
gtcgactcta gaggatccga caacaaagag tcaaccccac tgccacgtca agagcgaagc 60

gccacagcta agacaagagg gatcgatagc agttcatgat gtctaaactg ggagtcttgt 120

tgaccatctg tctgcttctg tttcccctta ctgctcttcc gatggatgga gatgaacctg 180

caaaccgacc tgtcgagcgt atgcaggaca acatttcatc tgagcagtat cccttgtttg 240

agaagagacg agattgttgc actccgccga agaaatgcaa agaccgacaa tgcaaacccc 300

agagatgttg cgctggacga taacgtgttg atgaccaact ttatcacggc tacgtcaagt 360

gtttagtgaa taagtaaaat gattgcagtc ttgctcagat ttgcttttgt gttttggtct 420

aaagatcaat gaccaaaccg ttgttttgat gcggattgtc atatatttct cgattccaat 480

ccaacactag atgatttaat cacgatagat taattttcta tcaatgcctt gatttttcgt 540

ctgtcatatc agttttgttt atatttattt tttcgtcact gtctacacaa acgcatgcat 600

gcacgcatgc acgcacacac gcacgcacgc tcgcacaaac atgcgcgcgc acgcacacac 660

acacacacac acacaaacac acacacaagc aatcacacaa ttattgacat tatttattta 720

ttcattgatg tatttgttat tcgtttgctt gtttttagaa tagtttgagg ccgtcttttt 780

ggatttattt gaactgcttt attgtatacg agtacttcgt gctttgaaac actgctgaaa 840

ataaaacaaa cactgacgta gc 862

<210> 98
<211> 75
<212> PRT
<213> Conus geographus

<400> 98
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Glu Pro Ala Asn Arg Pro
20 25 30

Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln Tyr Pro Leu Phe
35 40 45

Glu Lys Arg Arg Asp Cys Cys Thr Pro Pro Lys Lys Cys Lys Asp Arg
50 55 60

Gln Cys Lys Pro Gln Arg Cys Cys Ala Gly Arg
65 70 75

<210> 99
<211> 22
<212> PRT
<213> Conus geographus

<220>
<221> PEPTIDE
<222> (1)..(22)
<223> Xaa at residue 6, 7 and 17 is Pro or Hyp

<400> 99
Arg Asp Cys Cys Thr Xaa Xaa Lys Lys Cys Lys Asp Arg Gln Cys Lys
1 5 10 15

Xaa Gln Arg Cys Cys Ala
20

<210> 100
<211> 860
<212> DNA
<213> Conus geographus

<400> 100
ggccagacga caacaaagag tcaaccccac tgccacgtca agagcgaagc gccacagcta 60

agacaagagg gatcgatagc agttcatgat gtctaaactg ggagtcttgt tgaccatctg 120

tctgcttctg tttcccctta ctgctcttcc gatggatgga gatgaacctg caaaccgacc 180

tgtcgagcgt atgcaggaca acatttcatc tgagcagtat cccttgtttg agaagagacg 240

agattgttgc actccgccga ggaaatgcaa agaccgacga tgcaaaccca tgaaatgttg 300

cgctggacga taacgtgttg atgaccaact ttatcacggc tagctcagtg tttagtgaat 360

aagtaaaatg attgcagtct tgctcagatt gcttttgtgt tttggtctaa gatcaatgac 420

caaaccgttg ttttgatgcg gattgtcata tatttctcga ttccaatcca acactagatg 480

atttaatcac gatagattaa ttttctatca atgccttgat ttttcgtctg tcatatcagt 540

tttgtttata tttatttttt cgtcactgtc tacacaaacg catgcatgca cgcatgcacg 600

cacacacgca cgcacgctcg cacaaacatg cgcgcgcacg cacacacaca cacacacaca 660

aacacacaca cgaagcaatc acacaattag ttgacattat ttatttattc attgatgtat 720

ttgttattcg tttgcttgtt tttagaatag tttgaggccg tctttttgga tttatttgaa 780

ctgctttatt gtatacgagt acttcgtgct ttgaaacact gctgaaaata aaacaaacac 840

tgacgtagca aaaaaaaaaa 860

<210> 101
<211> 75
<212> PRT
<213> Conus geographus

<400> 101
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Glu Pro Ala Asn Arg Pro
20 25 30

Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln Tyr Pro Leu Phe
35 40 45

Glu Lys Arg Arg Asp Cys Cys Thr Pro Pro Arg Lys Cys Lys Asp Arg
50 55 60

Arg Cys Lys Pro Met Lys Cys Cys Ala Gly Arg
65 70 75

<210> 102
<211> 22
<212> PRT
<213> Conus geographus

<220>
<221> PEPTIDE
<222> (1)..(22)
<223> Xaa at residue 6, 7 and 17 is Pro or Hyp

<400> 102
Arg Asp Cys Cys Thr Xaa Xaa Arg Lys Cys Lys Asp Arg Arg Cys Lys
1 5 10 15

Xaa Met Lys Cys Cys Ala
20

<210> 103
<211> 22
<212> PRT
<213> Conus geographus

<220>
<221> PEPTIDE
<222> (1)..(22)
<223> Xaa at residue 6, 7 and 17 is Pro or Hyp

<400> 103
Arg Asp Cys Cys Thr Xaa Xaa Lys Lys Cys Lys Asp Arg Arg Cys Lys
1 5 10 15

Xaa Leu Lys Cys Cys Ala
20

<210> 104
<211> 321
<212> DNA
<213> Conus gloriamaris

<400> 104
ctcactatag gaattcgagc tcggtacacg ggatcgatag cagttcatga tgtctaaact 60

gggagccttg ttgaccatct gtctacttct gttttcccta actgctgttc cgctggatgg 120

agatcaacat gcagaccaac ctgcagagcg tctgcatgac cgccttccaa ctgaaaatca 180

tcccttatat gatcccgtca aacggtgttg cgatgattcg gaatgcgact attcttgctg 240

gccttgctgt atgtttggat aacctttgtt atcgcggcct cgataagtgt ctaatgaata 300

agtaaaacga ttgcagtagg c 321

<210> 105
<211> 71
<212> PRT
<213> Conus gloriamaris

<400> 105
Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
20 25 30

Ala Glu Arg Leu His Asp Arg Leu Pro Thr Glu Asn His Pro Leu Tyr
35 40 45

Asp Pro Val Lys Arg Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys
50 55 60

Trp Pro Cys Cys Met Phe Gly
65 70

<210> 106
<211> 17
<212> PRT
<213> Conus gloriamaris

<220>
<221> PEPTIDE
<222> (1)..(17)
<223> Xaa at residue is 6 Glu or gamma-carboxy Glu; Xaa at residue 13 i
s Pro or Hyp; Xaa at residue 12 is Trp or bromo-Trp; Xaa at resid
ue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr o
r O-phospho-Ty

<400> 106
Cys Cys Asp Asp Ser Xaa Cys Asp Xaa Ser Cys Xaa Xaa Cys Cys Met
1 5 10 15

Phe

<210> 107
<211> 257
<212> DNA
<213> Conus gloriamaris

<400> 107
gttcatgatg tctaaactgg gagtcttgtt gatcatctgt ctacttctgt ttccccttac 60

tgctgttccg ctggatggag atcaacctgc agaccgatat gcagagcgta tgcaggacga 120

catttcatct gaacatcatc ccatgtttga tgccgtcaga gggtgttgcc atctgttggc 180

atgccgcttc ggatgctcgc cttgttgttg gtgatcagct ttgttatcgc ggcctcatca 240

agtgactcta atgcaaa 257
<210> 108
<211> 69

<212> PRT
<213> Conus gloriamaris

<400> 108
Met Met Ser Lys Leu Gly Val Leu Leu Ile Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Tyr
20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu His His Pro Met Phe
35 40 45

Asp Ala Val Arg Gly Cys Cys His Leu Leu Ala Cys Arg Phe Gly Cys
50 55 60

Ser Pro Cys Cys Trp
65

<210> 109
<211> 17
<212> PRT
<213> Conus gloriamaris

<220>
<221> PEPTIDE
<222> (1)..(17)
<223> Xaa at residue 14 is Pro or Hyp; Xaa at residue 17 is Trp or brom
o-Tr

<400> 109
Gly Cys Cys His Leu Leu Ala Cys Arg Phe Gly Cys Ser Xaa Cys Cys
1 5 10 15

Xaa

<210> 110
<211> 471
<212> DNA
<213> Conus gloriamaris

<400> 110
gagacgacaa ggaacagtca accccacagc cacgccaaga gcagacagcc acagctacgt 60

gaagaagggt ggagagaggt tcgtgatgtt gaaaatggga gtggtgctat tcatcttcct 120

ggtactgttt cccctggcaa cgctccagct ggatgcagat caacctgtag aacgatatgc 180

ggagaacaaa cagctcctca acccagatga aaggagggaa atcatattgc atgctctggg 240

gacgcgatgc tgttcttggg atgtgtgcga ccacccgagt tgtacttgct gcggcggtta 300

gcgccgaaca tccatggcgc tgtgctgggc ggttttatcc aacaacgaca gcgtttgttg 360

atttcatgta tcattgcgcc cacgtctctt gtctaagaat gacgaacatg attgcactct 420

ggttcagatt tcgtgttctt ttctgacaat aaatgacaaa actccaaaaa a 471

<210> 111
<211> 71
<212> PRT
<213> Conus gloriamaris

<400> 111
Met Leu Lys Met Gly Val Val Leu Phe Ile Phe Leu Val Leu Phe Pro

1 5 10 15

Leu Ala Thr Leu Gln Leu Asp Ala Asp Gln Pro Val Glu Arg Tyr Ala
20 25 30

Glu Asn Lys Gln Leu Leu Asn Pro Asp Glu Arg Arg Glu Ile Ile Leu
35 40 45

His Ala Leu Gly Thr Arg Cys Cys Ser Trp Asp Val Cys Asp His Pro
50 55 60

Ser Cys Thr Cys Cys Gly Gly
65 70

<210> 112
<211> 16
<212> PRT
<213> Conus gloriamaris

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 10 is Pro or Hyp; Xaa at residue 4 is Trp or bromo -Tr

<400> 112
Cys Cys Ser Xaa Asp Val Cys Asp His Xaa Ser Cys Thr Cys Cys Gly
1 5 10 15

<210> 113
<211> 304
<212> DNA
<213> Conus laterculatus

<400> 113
cgacctcaag aaggatcgat agcagttcat gatgtctaaa ctgggagtct tgttgaccat 60

ctgtctgctt ctgtttcccc ttactgctct tccgatggat ggagatcaac ctgcagaccg 120

acctgcagag cgtatgcagg acgtttcatc tgaacagcat cccttgtatg atcccgtcaa 180

acggtgttgc gactggccat gcagcggatg catcccttgt tgctaatagt aacaacgtgt 240

tgataaccaa ctttcttacc acgactacgt caagtgtcta atgaataagt aaaatgattg 300

cagt 304

<210> 114
<211> 65
<212> PRT
<213> Conus laterculatus

<400> 114
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15
Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Pro
20 25 30

Ala Glu Arg Met Gln Asp Val Ser Ser Glu Gln His Pro Leu Tyr Asp
35 40 45

Pro Val Lys Arg Cys Cys Asp Trp Pro Cys Ser Gly Cys Ile Pro Cys
50 55 60

Cys

65

<210> 115
<211> 13
<212> PRT
<213> Conus laterculatus

<220>
<221> PEPTIDE
<222> (1)..(13)
<223> Xaa at residue 5 and 11 is Pro or Hyp; Xaa at residue 4 is Trp or bromo-Trp

<400> 115
Cys Cys Asp Xaa Xaa Cys Ser Gly Cys Ile Xaa Cys Cys
1 5 10

<210> 116
<211> 313
<212> DNA
<213> Conus laterculatus

<400> 116
cgacctcaag aaggatcgat agcagttcat gatgtctaaa ctgggagtct tgttgaccat 60

ctgtctgctt ctgtttcccc ttactgctct ggatggagat caacctgcag accgacttgc 120

agagcgtatg caggacgaca tttcatctga gcagcatccc tttgaaaaga gacgagactg 180

ttgcacacct ccgaagaaat gcagagaccg acaatgcaaa cctgcacgtt gttgcggagg 240

ataacgtgtt gatgaccaac tttgttatca cggctacgtc aagtgtctag tgaataagta 300

aaacgattgc agt 313

<210> 117
<211> 71
<212> PRT
<213> Conus laterculatus

<400> 117
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Asp Gly Asp Gln Pro Ala Asp Arg Leu Ala Glu
20 25 30

Arg Met Gln Asp Asp Ile Ser Ser Glu Gln His Pro Phe Glu Lys Arg
35 40 45

Arg Asp Cys Cys Thr Pro Pro Lys Lys Cys Arg Asp Arg Gln Cys Lys
50 55 60

Pro Ala Arg Cys Cys Gly Gly
65 70

<210> 118
<211> 22
<212> PRT
<213> Conus laterculatus

<220>
<221> PEPTIDE
<222> (1)..(22)
<223> Xaa at residue 6, 17 and 17 is Pro or Hyp

<400> 118
Arg Asp Cys Cys Thr Xaa Xaa Lys Lys Cys Arg Asp Arg Gln Cys Lys
1 5 10 15

Xaa Ala Arg Cys Cys Gly
20

<210> 119
<211> 314
<212> DNA
<213> Conus laterculatus

<400> 119
gggatcgata gcagttcatg atgtctaaac tgggagtctt gttgaccatc tgtctgcttc 60

tgtttcccct tactgctctt ccgatggatg gagatcaact tgcacgccga tctgcagagc 120

gtatgcagga caacatttca tctgagcagc atcacctctt tgaaaagaga cgaccaccat 180

gttgcaccta tgacgggagt tgcctaaaag aatcatgcat gcgtaaagct tgttgcggat 240

gataacgtgt tgatgaccaa ctttgttatc acggctactc aagtgtctaa tgaataagta 300

aaatgattgc agta 314

<210> 120
<211> 74
<212> PRT
<213> Conus laterculatus

<400> 120
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Leu Ala Arg Arg Ser
20 25 30

Ala Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His His Leu Phe
35 40 45

Glu Lys Arg Arg Pro Pro Cys Cys Thr Tyr Asp Gly Ser Cys Leu Lys
50 55 60

Glu Ser Cys Met Arg Lys Ala Cys Cys Gly
65 70

<210> 121
<211> 22
<212> PRT
<213> Conus laterculatus

<220>
<221> PEPTIDE
<222> (1)..(22)
<223> Xaa at residue 14 is Glu or gamma-carboxy Glu; Xaa at residue 2 a nd 3 is Pro or Hyp; Xaa at residue 7 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 121
Arg Xaa Xaa Cys Cys Thr Xaa Asp Gly Ser Cys Leu Lys Xaa Ser Cys
1 5 10 15

Met Arg Lys Ala Cys Cys
20

<210> 122
<211> 314
<212> DNA
<213> Conus laterculatus

<400> 122
gggatcgata gcagttcatg atgtctaaac tgggagtctt gttgaccacc tgtctgcttc 60

tgtttcccct tactgctctt ccgatggatg gagatcaact tgcacgccga cctgcagagc 120

gtatgcagga caacatttca tctgagcagc atcccttctt tgaaaggaga cgaccaccat 180

gttgcaccta tgacgggagt tgcctaaaag aatcatgcaa gcgtaaagct tgttgcggat 240

aataacgtgt tgatgaccaa ctttgttatc acggctactc aagtgtctaa tgaataagta 300

aaatgattgc agta 314

<210> 123
<211> 74
<212> PRT
<213> Conus laterculatus

<400> 123
Met Met Ser Lys Leu Gly Val Leu Leu Thr Thr Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Leu Ala Arg Arg Pro
20 25 30

Ala Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe
35 40 45

Glu Arg Arg Arg Pro Pro Cys Cys Thr Tyr Asp Gly Ser Cys Leu Lys
50 55 60

Glu Ser Cys Lys Arg Lys Ala Cys Cys Gly
65 70

<210> 124
<211> 22
<212> PRT
<213> Conus laterculatus

<220>
<221> PEPTIDE
<222> (1)..(22)
<223> Xaa at residue 14 is Glu or gamma-carboxy Glu; Xaa at residue 2 a
nd 3 is Pro or Hyp; Xaa at residue7 is Tyr, 125I-Tyr, mono-iodo-
Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 124
Arg Xaa Xaa Cys Cys Thr Xaa Asp Gly Ser Cys Leu Lys Xaa Ser Cys
1 5 10 15

Lys Arg Lys Ala Cys Cys
20

<210> 125
<211> 247
<212> DNA
<213> Conus leopardus

<400> 125

ggatccatga tgtctaaact gggagtcttg ttgaccgtct gtctgcttct gtttcccctt 60

actgctcttc ggctggttgg agatcaacct gcagagcgac ctgcaaagcg tacgcaggac 120

gacattccag atggacagca tccgttaaat gataggcaga taaactgttg cccgtggcca 180

tgccctagta catgccgcca tcaatgctgc cattaatgat aacgtgttga tgaccaactt 240

tctcgag 247

<210> 126
<211> 71
<212> PRT
<213> Conus leopardus

<400> 126
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Val Cys Leu Leu
1 5 10 15

Leu Phe Pro Leu Thr Ala Leu Arg Leu Val Gly Asp Gln Pro Ala Glu
20 25 30

Arg Pro Ala Lys Arg Thr Gln Asp Asp Ile Pro Asp Gly Gln His Pro
35 40 45

Leu Asn Asp Arg Gln Ile Asn Cys Cys Pro Trp Pro Cys Pro Ser Thr
50 55 60

Cys Arg His Gln Cys Cys His
65 70

<210> 127
<211> 19
<212> PRT
<213> Conus leopardus

<220>
<221> PEPTIDE
<222> (1)..(19)
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6, 8 and 10 i
s Pro or Hyp; Xaa at residue 7 is Trp or bromo-Tr

<400> 127
Xaa Ile Asn Cys Cys Xaa Xaa Xaa Cys Xaa Ser Thr Cys Arg His Gln
1 5 10 15

Cys Cys His

<210> 128
<211> 244
<212> DNA
<213> Conus lividus

<400> 128
ggatccatga tgtctaaact gggagtcttg ttgaccgtct gtctgcttct gtttcccctt 60

actgctcttc ggctggttag agatcaacct gcagagcgac ctgcaaagcg tacgcaggac 120

gacattccaa atggacagga tccgttaatt gataggcaga taaattgttg cccttggcca 180

tgccctgatt catgccacta tcaatgctgc cactgataac gtgttgatga ccaactttct 240

cgag 244

<210> 129

<211> 71
<212> PRT
<213> Conus lividus

<400> 129
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Val Cys Leu Leu
1 5 10 15

Leu Phe Pro Leu Thr Ala Leu Arg Leu Val Arg Asp Gln Pro Ala Glu
20 25 30

Arg Pro Ala Lys Arg Thr Gln Asp Asp Ile Pro Asn Gly Gln Asp Pro
35 40 45

Leu Ile Asp Arg Gln Ile Asn Cys Cys Pro Trp Pro Cys Pro Asp Ser
50 55 60

Cys His Tyr Gln Cys Cys His
65 70

<210> 130
<211> 19
<212> PRT
<213> Conus lividus

<220>
<221> PEPTIDE
<222> (1)..(19)
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6, 8 and 10 i s Pro or Hyp; Xaa at residue 7 is Trp or bromo-Trp; Xaa at residu e 15 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr o r O-phospho-Ty

<400> 130
Xaa Ile Asn Cys Cys Xaa Xaa Xaa Cys Xaa Asp Ser Cys His Xaa Gln
1 5 10 15

Cys Cys His

<210> 131
<211> 275
<212> DNA
<213> Conus lynceus

<400> 131
aaggatcgat agcagttcat gatgtctaaa ctgggagtct tgttgaccat ctgtctgctt 60

ctgtttcccc ttactgctct tccgatggat ggagatcaat ctgcagaccg acttgcagag 120

cgtatgcagg acaacatttc atctgagcag catcccttct ttgaaaagag aggacgagac 180

tgttgcacac ctccgaggaa atgcagagac cgagcctgca aacctcaacg ttgttgcgga 240

ggataagctg ttgatgacca actttgttat acggc 275

<210> 132
<211> 75
<212> PRT
<213> Conus lynceus

<400> 132
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Ser Ala Asp Arg Leu

20 25 30

Ala Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe
35 40 45

Glu Lys Arg Gly Arg Asp Cys Cys Thr Pro Pro Arg Lys Cys Arg Asp
50 55 60

Arg Ala Cys Lys Pro Gln Arg Cys Cys Gly Gly
65 70 75

<210> 133
<211> 23
<212> PRT
<213> Conus lynceus

<220>
<221> PEPTIDE
<222> (1)..(23)
<223> Xaa at residue 7, 8 and 18 is Pro or Hyp

<400> 133
Gly Arg Asp Cys Cys Thr Xaa Xaa Arg Lys Cys Arg Asp Arg Ala Cys
1 5 10 15

Lys Xaa Gln Arg Cys Cys Gly
20

<210> 134
<211> 803
<212> DNA
<213> Conus magus

<400> 134
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct 60

gcttctgttt ccccttactg ctcttccgat ggatggagat gaacctgcaa accgacctgt 120

cgagcgtatg caggacaaca tttcatctga gcagtatccc ttgtttgaga agagacgaga 180

ttgttgcact ccgccgaaga aatgcaaaga ccgacaatgc aaaccccaga gatgttgcgc 240

tggacgataa cgtgttgatg accaacttta tcacggctac gtcaagtgtt tagtgaataa 300

gtaaaatgat tgcagtcttg ctcagatttg cttttgtgtt ttggtctaaa gatcaatgac 360

caaaccgttg ttttgatgcg gattgtcata tatttctcga ttccaatcca acactagatg 420

atttaatcac gatagattaa ttttctatca atgccttgat tttcgtctg tcatatcagt 480

tttgtttata tttatttttt cgtcactgtc tacacaaacg catgcatgca cgcatgcacg 540

cacacacgca cgcacgctcg cacaaacatg cgcgcgcacg cacacacaca cacacacaca 600

caaacacaca cacgaagcaa tcacacaatt agttgacatt atttatttat tcattgatgt 660

atttgttatt cgtttgcttg tttttagaat agtttgaggc cgtctttttg gatttatttg 720

aactgcttta ttgtatacga gtacttcgtg cggggaaaca ctgctgaaaa taaaacaaac 780

actgacgtag caaaaaaaaa aaa 803

<210> 135
<211> 75
<212> PRT

<213> Conus magus

<400> 135
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Glu Pro Ala Asn Arg Pro
20 25 30

Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln Tyr Pro Leu Phe
35 40 45

Glu Lys Arg Arg Asp Cys Cys Thr Pro Pro Lys Lys Cys Lys Asp Arg
50 55 60

Gln Cys Lys Pro Gln Arg Cys Cys Ala Gly Arg
65 70 75

<210> 136
<211> 22
<212> PRT
<213> Conus magus

<220>
<221> PEPTIDE
<222> (1)..(22)
<223> Xaa at residue 6 and 7 is Pro or Hyp
<400> 136
Arg Asp Cys Cys Thr Xaa Xaa Lys Lys Cys Lys Asp Arg Gln Cys Lys
1 5 10 15

Xaa Gln Arg Cys Cys Ala
20

<210> 137
<211> 656
<212> DNA
<213> Conus magus

<400> 137
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct 60

gcttctgttt ccccttactg ctcttccaat ggatggagat caacctgcag accaacctgc 120

agatcgtatg caggacgaca tttcatctga gcagtatccc ttgtttgata tgagaaaaag 180

gtgttgcggc cccggcggtt catgccccgt atatttcaga gacaatttta tttgtggttg 240

ttgttaaatg acaacgtgtc gatgaccaac ttcattatca cgactacgcc aagtgtctaa 300

tgaataaata aaatgattgc agtctcgctc agatttgctt ttgtattttg gtctaaagat 360

caatgaccaa accgttgttt tggtgtggat tttcatatat ttctcgagtc ctatccaaca 420

ctagatgatt taatcacgat agatctgatt tttttatcaa aggcttggtt tttcgtctgt 480

cacatcagtt ttgtttatat ttaatttttc gtcactgatt acacacacgc atgaacgcac 540

agagtactaa cacatacaca cacacacaca cacacacaca cacacacaca cacacacaca 600

cacacacaca cacgcgcgcg cgcggcgcca tctagtagcg ccgcgacgac acacac 656

<210> 138
<211> 74
<212> PRT

<213> Conus magus

<400> 138
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro
20 25 30

Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe
35 40 45

Asp Met Arg Lys Arg Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr
50 55 60

Phe Arg Asp Asn Phe Ile Cys Gly Cys Cys
65 70

<210> 139
<211> 21
<212> PRT
<213> Conus magus

<220>
<221> PEPTIDE
<222> (1)..(21)
<223> Xaa at residue 4 and 9 is Pro or Hyp; Xaa at residue is 11 Tyr, 1
25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 139
Cys Cys Gly Xaa Gly Gly Ser Cys Xaa Val Xaa Phe Arg Asp Asn Phe
1 5 10 15

Ile Cys Gly Cys Cys
20

<210> 140
<211> 594
<212> DNA
<213> Conus magus

<400> 140
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgttt 60

gcttctgttt ccccttactg ctcttccgag ggatggagat caatctgtag accgacctgc 120

agagcgtatg caggacgaca tttcatctga gctgcatccc ttgtcaatca gaaaaagaat 180

gtgttgcggc gagagtgcgc catgccccag ctatttcaga aacagtcaga tttgtcattg 240

ttgttaaatg acaacgtgtc gatgaccacc ttcgttatca cgactaatga taagtaaaat 300

gattgcagtc tcgctcagat ttgcttttgt attttggtct aaagatcaat gaccaaaccg 360

ttgttttgat gtggattttc atatatttct cgagtcctat ccaacactag atgatttaat 420

cacgatagat ctgatttttt tatcaaagcc ttggtttttc gtctgtcaca tcagttttgt 480

ttatatttaa tttttcgtca ctgattacac acacgcatga acgcacagac gtactaacac 540

atacacacac acacacacac acacacacac acacacacac acacacacac acac 594

<210> 141
<211> 74

<212> PRT
<213> Conus magus

<400> 141
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Arg Asp Gly Asp Gln Ser Val Asp Arg Pro
20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Leu His Pro Leu Ser
35 40 45

Ile Arg Lys Arg Met Cys Cys Gly Glu Ser Ala Pro Cys Pro Ser Tyr
50 55 60

Phe Arg Asn Ser Gln Ile Cys His Cys Cys
65 70

<210> 142
<211> 22
<212> PRT
<213> Conus magus

<220>
<221> PEPTIDE
<222> (1)..(22)
<223> Xaa at residue 5 is Glu or gamma-carboxy Glu; Xaa at residue 8 an
d 10 is Pro or Hyp; Xaa at residue 12 is Tyr, 125I-Tyr, mono-iodo
-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 142
Met Cys Cys Gly Xaa Ser Ala Xaa Cys Xaa Ser Xaa Phe Arg Asn Ser
1 5 10 15

Gln Ile Cys His Cys Cys
20

<210> 143
<211> 501
<212> DNA
<213> Conus magus

<400> 143
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct 60

gcttctgttt cccottactg ctcttccaat ggatggagat caacctgcag accaacctgc 120

agatcgtatg caggacgaca tttcatctga gcagtatccc ttgtttgata agagacaaaa 180

gtgttgcggc cccggcggtt catgccccgt atatttcaca gacaatttta tttgtggttg 240

ttgttaaatg acaacgtgtc gatgaccaac ttcattatca cgactacgcc aagtgtctaa 300

tgaataaata aaatgattgc agtctcgctc agatttgctt ttgtatttgg tctaaagatc 360

aatgaccaaa ccgttgtttt ggtgctggat tttcatatat ttctcgattc ctatccaaca 420

ctagatgatt taatcacgat agatctgatt tttttatcaa tgccttaatt ttttgctctg 480

tcatatcagt tttgtttata t 501

<210> 144
<211> 74
<212> PRT

<213> Conus magus

<400> 144
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro
20 25 30

Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe
35 40 45

Asp Lys Arg Gln Lys Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr
50 55 60

Phe Thr Asp Asn Phe Ile Cys Gly Cys Cys
65 70

<210> 145
<211> 23
<212> PRT
<213> Conus magus

<220>
<221> PEPTIDE
<222> (1)..(23)
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6 and 11 is P
ro or Hyp; Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-
iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 145
Xaa Lys Cys Cys Gly Xaa Gly Gly Ser Cys Xaa Val Xaa Phe Thr Asp
1 5 10 15

Asn Phe Ile Cys Gly Cys Cys
20

<210> 146
<211> 454
<212> DNA
<213> Conus magus

<400> 146
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct 60

gcttctgttt ccccttactg ctcttccaat ggatggagat caacctgcag accaacctgc 120

agatcgtatg caggacgaca tttcatctga gcagtatccc ttgtttgata agagacaaaa 180

gtgttgcggc cccggcggtt catgccccgt atatttcaga gacaatttta tttgtggttg 240

ttgttaaatg acaacgtgtc gatgaccatc ttcattatca cgactacgcc aagtgtctaa 300

tgaataaata aaatgattgc agtctcgctc agatttgctt ttgtattttg gtctaaagat 360

caatgaccaa accgttgttt tggtgtggat tttcatatat ttctcgattc ctatccaaca 420

ctagatgatt taatcacgat agatctgatt tttt 454

<210> 147
<211> 74
<212> PRT
<213> Conus magus

<400> 147

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro
20 25 30

Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe
35 40 45

Asp Lys Arg Gln Lys Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr
50 55 60
Phe Arg Asp Asn Phe Ile Cys Gly Cys Cys
65 70

<210> 148
<211> 23
<212> PRT
<213> Conus magus

<220>
<221> PEPTIDE
<222> (1)..(23)
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6 and 11 is P ro or Hyp; Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 148
Xaa Lys Cys Cys Gly Xaa Gly Gly Ser Cys Xaa Val Xaa Phe Arg Asp
1 5 10 15

Asn Phe Ile Cys Gly Cys Cys
20

<210> 149
<211> 22
<212> PRT
<213> Conus magus

<220>
<221> PEPTIDE
<222> (1)..(22)
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 10 and 20 is Pro or Hyp; Xaa at residue 12 is Tyr, 125I-Tyr, mono-iodo-Tyr, di -iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 149
Xaa Lys Cys Cys Ser Gly Gly Ser Cys Xaa Leu Xaa Phe Arg Asp Arg
1 5 10 15

Leu Ile Cys Xaa Cys Cys
20

<210> 150
<211> 19
<212> PRT
<213> Conus marmoreus

<220>
<221> PEPTIDE
<222> (1)..(19)
<223> Xaa at residue 16 is Pro or Hyp

<400> 150
Ser Lys Gln Cys Cys His Leu Ala Ala Cys Arg Phe Gly Cys Thr Xaa
1 5 10 15

Cys Cys Asn

<210> 151
<211> 321
<212> DNA
<213> Conus marmoreus
<400> 151
caagaaggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct 60

gcttctgttt cccgttactg ctcttccgat ggatggtgat caacctgcag accgacttgt 120

agagcgtatg caggacaaca tttcatctga gcagcatccc ttctttgaaa agagaagagg 180

aggctgttgc acacctccga ggaaatgcaa agaccgagcc tgcaaacctg cacgttgctg 240

cggcccagga taacgtgttg atgaccaact ttgttatcac ggctacgtca agtgtctagt 300

gaataagtaa aacgattgca g 321

<210> 152
<211> 76
<212> PRT
<213> Conus marmoreus

<400> 152
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Val Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Leu
20 25 30

Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe
35 40 45

Glu Lys Arg Arg Gly Gly Cys Cys Thr Pro Pro Arg Lys Cys Lys Asp
50 55 60

Arg Ala Cys Lys Pro Ala Arg Cys Cys Gly Pro Gly
65 70 75

<210> 153
<211> 24
<212> PRT
<213> Conus marmoreus

<220>
<221> PEPTIDE
<222> (1)..(24)
<223> Xaa at residue 3, 8, 18 and 24 is Pro or Hyp

<400> 153
Arg Gly Gly Cys Cys Thr Xaa Xaa Arg Lys Cys Lys Asp Arg Ala Cys
1 5 10 15

Lys Xaa Ala Arg Cys Cys Gly Xaa
20

<210> 154
<211> 296
<212> DNA
<213> Conus marmoreus

<400> 154
gagctcggta ccccgacctc aagagggatc gatagcagtt catgatgtct aaactgggaa 60

tcttgttgac catctgtcta cttctatttc cccttactgc tgttccgctg gatggagatc 120

aacctgcaga ccgacctgca gagcgtatgc aggacgacat ttcatctgaa catcatccct 180

tttttgatcc cgtcaaacgg tgttgcaggt tatcatgcgg cctgggatgc cacccttgtt 240

gtggatgacc agctttgtta tcgcggcctc atcaagtgtc taatgaataa gtaaaa 296

<210> 155
<211> 68
<212> PRT
<213> Conus marmoreus

<400> 155
Met Met Ser Lys Leu Gly Ile Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro
20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu His His Pro Phe Phe
35 40 45

Asp Pro Val Lys Arg Cys Cys Arg Leu Ser Cys Gly Leu Gly Cys His
50 55 60

Pro Cys Cys Gly
65

<210> 156
<211> 14
<212> PRT
<213> Conus marmoreus

<220>
<221> PEPTIDE
<222> (1)..(14)
<223> Xaa at residue 12 is Pro or Hyp

<400> 156
Cys Cys Arg Leu Ser Cys Gly Leu Gly Cys His Xaa Cys Cys
1 5 10

<210> 157
<211> 355
<212> DNA
<213> Conus marmoreus

<400> 157
ggcctacacc aagcttgcat gcctgcaggt cgactctaga ggatccccga tcgatagcag 60

ttcatgatgt ctagactggg agtcttgttg accatctgtc tacttctgtt tcccccttact 120

gctgttccgc tggatggaga tcaacctgcg gaccgacctg cagagcgcct gcaggacgac 180

atttcatctg aacatcatcc ccattttgat tccggcagag agtgttgcgg ttcgttcgca 240

tgccgctttg gatgcgtgcc ttgttgtgta tgaccagctt tgttatcacg gcctcatcga 300

gtgtctaatg aataagtaaa acgattgcag taggcgggta ccgagctcga attcc 355

<210> 158
<211> 69
<212> PRT

<213> Conus marmoreus

<400> 158
Met Met Ser Arg Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro
20 25 30

Ala Glu Arg Leu Gln Asp Asp Ile Ser Ser Glu His His Pro His Phe
35 40 45

Asp Ser Gly Arg Glu Cys Cys Gly Ser Phe Ala Cys Arg Phe Gly Cys
50 55 60

Val Pro Cys Cys Val
65

<210> 159
<211> 17
<212> PRT
<213> Conus marmoreus

<220>
<221> PEPTIDE
<222> (1)..(17)
<223> Xaa at residue 1 is Glu or gamma-carboxy Glu; Xaa at residue 14 i
s Pro or Hy

<400> 159
Xaa Cys Cys Gly Ser Phe Ala Cys Arg Phe Gly Cys Val Xaa Cys Cys
1 5 10 15

Val

<210> 160
<211> 295
<212> DNA
<213> Conus marmoreus

<400> 160
cgacctcaag agggatcgat agcagttcat gatgtctaaa ctgggagtct tgttgaccat 60

ctgtctactt ctatttcccc ttactgctgt tccgctggat ggagaccaac ctgcagaccg 120

acctgcagag cgtatgcagg acgacatttc atctgaacgt catccttttt ttgatcgcag 180

caaacagtgt tgccatctgc cggcatgccg cttcggatgt acgccttgtt gttggtgatc 240

agctttgtta tcgcgtcctc atcaagtgtc taatgaataa gtaaaatgat tgcag 295

<210> 161
<211> 67
<212> PRT
<213> Conus marmoreus

<400> 161
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro
20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser His Pro Phe Phe Asp Arg
35 40 45

Ser Lys Gln Cys Cys His Leu Pro Ala Cys Arg Phe Gly Cys Thr Pro
50 55 60

Cys Cys Trp
65

<210> 162
<211> 19
<212> PRT
<213> Conus marmoreus

<220>
<221> PEPTIDE
<222> (1)..(19)
<223> Xaa at residue 8 and 16 is Pro or Hyp; Xaa at residue 19 is Trp o
r bromo-Tr

<400> 162
Ser Lys Gln Cys Cys His Leu Xaa Ala Cys Arg Phe Gly Cys Thr Xaa
1 5 10 15

Cys Cys Xaa

<210> 163
<211> 235
<212> DNA
<213> Conus marmoreus

<400> 163
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt 60

actgctcttc cgctggatgg agatcaacct gcagaccaac gtgcagagcg tacgcaggcc 120

gagaagcatt ccttgcctga tccgagaatg ggctgttgcc cgtttccatg caaaaccagt 180

tgcactactt tgtgttgcgg gtgatgataa cgtgttgatg accaactttc tcgag 235

<210> 164
<211> 67
<212> PRT
<213> Conus marmoreus

<400> 164
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
1 5 10 15

Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp
20 25 30

Gln Arg Ala Glu Arg Thr Gln Ala Glu Lys His Ser Leu Pro Asp Pro
35 40 45

Arg Met Gly Cys Cys Pro Phe Pro Cys Lys Thr Ser Cys Thr Thr Leu
50 55 60

Cys Cys Gly
65

<210> 165
<211> 17
<212> PRT
<213> Conus marmoreus

<220>

<221> PEPTIDE
<222> (1)..(17)
<223> Xaa at residue 5 and 7 is Pro or Hyp

<400> 165
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Met Gly Cys Cys Xaa Phe Xaa Cys Lys Thr Ser Cys Thr Thr Leu Cys
1               5                   10                  15

Cys
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<210> 166
<211> 16
<212> PRT
<213> Conus marmoreus

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 4 and 6 is Trp or bromo-Trp

<400> 166
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Cys Cys His Xaa Asn Xaa Cys Asp His Leu Cys Ser Cys Cys Gly Ser
1               5                   10                  15
```

<210> 167
<211> 357
<212> DNA
<213> Conus marmoreus

<400> 167
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gccaagcttg catgcctgca ggatgactct agaggatccc cacctcaaga gggatcgata    60

gcagttcatg atgtctaaac tgggagtctt gttgaccatc tgtctacttc tgtttgccct   120

tactgctgtt ccgctggatg gagatcaacc tgcagaccga cctgcagaac gtatgcagga   180

cgacatttca tctgaacgtc atcccatgtt tgatgccgtc agagattgtt gcccgttgcc   240

ggcatgcccc tttggatgca acccttgttg tggatgacca gctttgttat cgggacctca   300

tcaagtgtct aatgaataag taaaaaacga ttcgagtggg taccgagctc gaattcc      357
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<210> 168
<211> 67
<212> PRT
<213> Conus marmoreus

<400> 168
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Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1               5                   10                  15

Ala Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro
            20                  25                  30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser His Pro Met Phe Asp Ala
        35                  40                  45

Val Arg Asp Cys Cys Pro Leu Pro Ala Cys Pro Phe Gly Cys Asn Pro
    50                  55                  60

Cys Cys Gly
65
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<210> 169
<211> 16

<212> PRT
<213> Conus marmoreus

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 4, 6, 9 and 14 is Pro or Hyp

<400> 169
Asp Cys Cys Xaa Leu Xaa Ala Cys Xaa Phe Gly Cys Asn Xaa Cys Cys
1 5 10 15

<210> 170
<211> 16
<212> PRT
<213> Conus marmoreus

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 4 and 13 is Pro or Hyp

<400> 170
Cys Cys Ala Xaa Ser Ala Cys Arg Leu Gly Cys Arg Xaa Cys Cys Arg
1 5 10 15

<210> 171
<211> 16
<212> PRT
<213> Conus marmoreus

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 4 and 13 is Pro or Hyp

<400> 171
Cys Cys Ala Xaa Ser Ala Cys Arg Leu Gly Cys Arg Xaa Cys Cys Arg
1 5 10 15

<210> 172
<211> 16
<212> PRT
<213> Conus marmoreus

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 4 and 13 is Pro or Hyp

<400> 172
Cys Cys Ala Xaa Ser Ala Cys Arg Leu Gly Cys Arg Xaa Cys Cys Arg
1 5 10 15

<210> 173
<211> 17
<212> PRT
<213> Conus marmoreus

<220>
<221> PEPTIDE
<222> (1)..(17)
<223> Xaa at residue 14 is Pro or Hyp

<400> 173

Gly Cys Cys Gly Ser Phe Ala Cys Arg Phe Gly Cys Val Xaa Cys Cys
1 5 10 15

Val

<210> 174
<211> 244
<212> DNA
<213> Conus nobilis

<400> 174
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctacttct gtttcccctt 60

actgctcttc cgctggatga agatcaaccg gtacaccgac ctgcagagcg tatgcaggac 120

atttcatctg atcaacatct cttctttgat ctcatcaaac ggtgctgcga gttgccatgc 180

gggccaggct tttgcgtccc ttgttgctga catcaataac gtgttgatga ccaactttct 240

cgag 244

<210> 175
<211> 69
<212> PRT
<213> Conus nobilis

<400> 175
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
1 5 10 15

Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Val His
20 25 30

Arg Pro Ala Glu Arg Met Gln Asp Ile Ser Ser Asp Gln His Leu Phe
35 40 45

Phe Asp Leu Ile Lys Arg Cys Cys Glu Leu Pro Cys Gly Pro Gly Phe
50 55 60

Cys Val Pro Cys Cys
65

<210> 176
<211> 15
<212> PRT
<213> Conus nobilis

<220>
<221> PEPTIDE
<222> (1)..(15)
<223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 5, 8 adn 13 is Pro or Hy

<400> 176
Cys Cys Xaa Leu Xaa Cys Gly Xaa Gly Phe Cys Val Xaa Cys Cys
1 5 10 15

<210> 177
<211> 262
<212> DNA
<213> Conus nobilis

<400> 177
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctacttct gtttcccctt 60

actgcttttc cgatggatgg agatcaacct gcagaccaac ctgcagatcg tatgcaggac 120

gacatttcat ctgagcagta tcccttgttt gataagagac aaaagtgttg cactgggaag 180

aaggggtcat gctccggcaa agcatgcaaa aatctcaaat gttgctctgg acgataacgt 240

gttgatgacc aactttctcg ag 262

<210> 178
<211> 78
<212> PRT
<213> Conus nobilis

<400> 178
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
1 5 10 15

Leu Phe Pro Leu Thr Ala Phe Pro Met Asp Gly Asp Gln Pro Ala Asp
20 25 30

Gln Pro Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro
35 40 45

Leu Phe Asp Lys Arg Gln Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys
50 55 60

Ser Gly Lys Ala Cys Lys Asn Leu Lys Cys Cys Ser Gly Arg
65 70 75

<210> 179
<211> 23
<212> PRT
<213> Conus nobilis

<220>
<221> PEPTIDE
<222> (1)..(23)
<223> Xaa at residue 1 is Gln or pyro-Glu

<400> 179
Xaa Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys Ala Cys
1 5 10 15

Lys Asn Leu Lys Cys Cys Ser
20

<210> 180
<211> 238
<212> DNA
<213> Conus pulicarius

<400> 180
ggatccatga tgtctaaact gggagttttg ttgaccatct gtctgcttct gtttcccctt 60

actgctgttc cgctggatgg agatcaacct gcagaccgac ctgcagagcg tatgcaggac 120

attgcaactg aacagcatcc cttctttgat cccgtcaaac ggtgttgcaa cagctgttac 180

atgggatgca tcccttgttg cttctagtaa taacgtgttg atgaccaact ttctcgag 238

<210> 181
<211> 68
<212> PRT
<213> Conus pulicarius

<400> 181
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
1 5 10 15

Leu Phe Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp
20 25 30

Arg Pro Ala Glu Arg Met Gln Asp Ile Ala Thr Glu Gln His Pro Phe
35 40 45

Phe Asp Pro Val Lys Arg Cys Cys Asn Ser Cys Tyr Met Gly Cys Ile
50 55 60

Pro Cys Cys Phe
65

<210> 182
<211> 14
<212> PRT
<213> Conus pulicarius

<220>
<221> PEPTIDE
<222> (1)..(14)
<223> Xaa at residue 11 is Pro or Hyp; Xaa at residue 5 is Tyr, 125I-Ty
r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 182
Cys Cys Asn Ser Cys Xaa Met Gly Cys Ile Xaa Cys Cys Phe
1 5 10

<210> 183
<211> 238
<212> DNA
<213> Conus quercinus

<400> 183
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt 60

acagctcttc agctggatgg agatcaacct gcagaccgac ctgcagagcg tacgcaggac 120

attgcatctg aacagtatcg aaagtttgat cagagacaga ggtgttgcca gtggccatgc 180

cccggtagtt gcagatgctg ccgtactggt taacgtgttg atgaccaact ttctcgag 238

<210> 184
<211> 70
<212> PRT
<213> Conus quercinus

<400> 184
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
1 5 10 15

Leu Phe Pro Leu Thr Ala Leu Gln Leu Asp Gly Asp Gln Pro Ala Asp
20 25 30

Arg Pro Ala Glu Arg Thr Gln Asp Ile Ala Ser Glu Gln Tyr Arg Lys
35 40 45

Phe Asp Gln Arg Gln Arg Cys Cys Gln Trp Pro Cys Pro Gly Ser Cys
50 55 60

Arg Cys Cys Arg Thr Gly
65 70

<210> 185
<211> 17
<212> PRT
<213> Conus quercinus

<220>
<221> PEPTIDE
<222> (1)..(17)
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 7 and 9 is Pr
o or Hyp; Xaa at residue 6 is Trp or bromo-Tr

<400> 185
Xaa Arg Cys Cys Gln Xaa Xaa Cys Xaa Gly Ser Cys Arg Cys Cys Arg
1 5 10 15

Thr

<210> 186
<211> 15
<212> PRT
<213> Conus quercinus

<220>
<221> PEPTIDE
<222> (1)..(15)
<223> Xaa at residue 11 and 14 is Pro or Hyp

<400> 186
Cys Cys Ser Gln Asp Cys Leu Val Cys Ile Xaa Cys Cys Xaa Asn
1 5 10 15

<210> 187
<211> 15
<212> PRT
<213> Conus quercinus

<220>
<221> PEPTIDE
<222> (1)..(15)
<223> Xaa at residue 11 14 is Pro or Hyp; Xaa at residue 7 is Trp or br
omo-Tr

<400> 187
Cys Cys Ser Arg His Cys Xaa Val Cys Ile Xaa Cys Cys Xaa Asn
1 5 10 15

<210> 188
<211> 323
<212> DNA
<213> Conus radiatus

<400> 188
tcaagaagga tcgatagcag ttcatgatgt ctaaactggg agtcttgttg accatctgtc 60

tgcttctgtt tccccttact gctcttccga tggatggaga tcaacctgta gaccgacttg 120

cagagcgtat gcaggacaac atttcatctg agcagcatac cttctttgaa aagagactac 180

catcgtgttg ctcccttaac ttgcggcttt gcccagtacc agcatgcaaa cgtaaccctt 240

gttgcacagg ataacgtgtt gatgaccaac tttgttatca cggctacgtc aagtgtctag 300

tgaataagta aaacgattgc agt 323

<210> 189
<211> 76
<212> PRT
<213> Conus radiatus

<400> 189
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Val Asp Arg Leu
20 25 30

Ala Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Thr Phe Phe
35 40 45

Glu Lys Arg Leu Pro Ser Cys Cys Ser Leu Asn Leu Arg Leu Cys Pro
50 55 60

Val Pro Ala Cys Lys Arg Asn Pro Cys Cys Thr Gly
65 70 75

<210> 190
<211> 24
<212> PRT
<213> Conus radiatus

<220>
<221> PEPTIDE
<222> (1)..(24)
<223> Xaa at residue 2, 13, 15 and 21 is Pro or Hyp

<400> 190
Leu Xaa Ser Cys Cys Ser Leu Asn Leu Arg Leu Cys Xaa Val Xaa Ala
1 5 10 15

Cys Lys Arg Asn Xaa Cys Cys Thr
20

<210> 191
<211> 336
<212> DNA
<213> Conus radiatus

<400> 191
aggtcgactc tagaggatcc ccaaggatcg atagcagttc atgatgtcta aactgggagt 60

cttgttgacc atctgtctgc ttctgtttcc ccttactgct cttccgatgg atggagatca 120

acctgcagac cgacttgcag agcgtatgca ggacgacatt tcatctgagc agcatccctt 180

ctttaaaaag agacaacaaa gatgttgcac cgttaagagg atttgtccag taccagcatg 240

cagaagtaaa ccttgttgca aatcataacg tattgatgac caactttgtt atcacggcta 300

cgtcaagtgt ctagtgaata agtaaaatga ttgcag 336

<210> 192
<211> 75
<212> PRT
<213> Conus radiatus

<400> 192
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Leu
20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln His Pro Phe Phe
35 40 45

Lys Lys Arg Gln Gln Arg Cys Cys Thr Val Lys Arg Ile Cys Pro Val
50 55 60

Pro Ala Cys Arg Ser Lys Pro Cys Cys Lys Ser
65 70 75

<210> 193
<211> 24
<212> PRT
<213> Conus radiatus

<220>
<221> PEPTIDE
<222> (1)..(24)
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 12, 14 and 20 is Pro or Hy

<400> 193
Xaa Gln Arg Cys Cys Thr Val Lys Arg Ile Cys Xaa Val Xaa Ala Cys
1 5 10 15

Arg Ser Lys Xaa Cys Cys Lys Ser
20

<210> 194
<211> 326
<212> DNA
<213> Conus radiatus

<400> 194
acctcaagaa ggatcgatag cagttcatga tgtctaaact gggagtcttg ttgaccatct 60

gtctgcttct gtttcccgtt actgctcttc cgatggatgg tgatcaacct gcagaccgac 120

ttgtagagcg tatgcaggac aacatttcat ctgagcagca tcccttcttt gaaaagagaa 180

gaggaggctg ttgcacacct ccgaggaaat gcaaagaccg agcctgcaaa cctgcacgtt 240

gctgcggccc aggataacgt gttgatgacc aactttgtta tcacggctac gtcaagtgtc 300

tagtgaataa gtaaaacgat tgcagt 326

<210> 195
<211> 76
<212> PRT
<213> Conus radiatus

<400> 195
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Val Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Leu
20 25 30

Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe
35 40 45

Glu Lys Arg Arg Gly Gly Cys Cys Thr Pro Pro Arg Lys Cys Lys Asp
50 55 60

```
Arg Ala Cys Lys Pro Ala Arg Cys Cys Gly Pro Gly
65                  70                  75

&lt;210&gt;  196
&lt;211&gt;  24
&lt;212&gt;  PRT
&lt;213&gt;  Conus radiatus

&lt;220&gt;
&lt;221&gt;  PEPTIDE
&lt;222&gt;  (1)..(24)
&lt;223&gt;  Xaa at residue 7, 8, 18 and 24 is Pro or Hyp

&lt;400&gt;  196
Arg Gly Gly Cys Cys Thr Xaa Xaa Arg Lys Cys Lys Asp Arg Ala Cys
1               5                   10                  15

Lys Xaa Ala Arg Cys Cys Gly Xaa
            20
&lt;210&gt;  197
&lt;211&gt;  238
&lt;212&gt;  DNA
&lt;213&gt;  Conus rattus

&lt;400&gt;  197
ggatccatga tgtctaaact gggagtcttg gtgaccatct gcctgcttct gttccctctt      60

gctgcttttc cactggatgg agatcaacct gcagaccacc ctgcaaagcg tacgcaagat     120

gacagttcag ctgccctgat caatgcctgg cttgatgaat cccagacttg ctgcagtaac     180

tgcggtgaag attgtgatgg ttgttgccag taacgtgttg atgaccaact ttctcgag       238

&lt;210&gt;  198
&lt;211&gt;  70
&lt;212&gt;  PRT
&lt;213&gt;  Conus rattus

&lt;400&gt;  198
Gly Ser Met Met Ser Lys Leu Gly Val Leu Val Thr Ile Cys Leu Leu
1               5                   10                  15

Leu Phe Pro Leu Ala Ala Phe Pro Leu Asp Gly Asp Gln Pro Ala Asp
            20                  25                  30

His Pro Ala Lys Arg Thr Gln Asp Asp Ser Ser Ala Ala Leu Ile Asn
        35                  40                  45

Ala Trp Leu Asp Glu Ser Gln Thr Cys Cys Ser Asn Cys Gly Glu Asp
    50                  55                  60

Cys Asp Gly Cys Cys Gln
65                  70

&lt;210&gt;  199
&lt;211&gt;  16
&lt;212&gt;  PRT
&lt;213&gt;  Conus rattus

&lt;220&gt;
&lt;221&gt;  PEPTIDE
&lt;222&gt;  (1)..(16)
&lt;223&gt;  Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 9 is Glu or g
       amma-carboxy Gl
```

<400> 199
Xaa Thr Cys Cys Ser Asn Cys Gly Xaa Asp Cys Asp Gly Cys Cys Gln
1 5 10 15

<210> 200
<211> 327
<212> DNA
<213> Conus stercusmuscarum

<400> 200
gacctcaaga gggatcgata gcagttcgtg atgtctaaac tgggagtctt gttgaccatc 60

tgtctgcttc tgtttcctct tactgctctt ccgatggatg gagatcaacc tgcagaccaa 120

cctgcagatc gtatgcagga cgacatttca tctgagcagt atcccttgtt tgataagaga 180
caaaagtgtt gcactgggaa gaaggggtca tgctccggca aagcatgcaa aaatctcaaa 240

tgttgctctg gacgataacg tgttgatgac caactttgtt atcacggcta cgtcaagtgt 300

ctaatgaata agtaaaacga ttgcagt 327

<210> 201
<211> 75
<212> PRT
<213> Conus stercusmuscarum

<400> 201
Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe Pro
1 5 10 15

Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro Ala
20 25 30

Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe Asp
35 40 45

Lys Arg Gln Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys
50 55 60

Ala Cys Lys Asn Leu Lys Cys Cys Ser Gly Arg
65 70 75

<210> 202
<211> 23
<212> PRT
<213> Conus stercusmuscarum

<220>
<221> PEPTIDE
<222> (1)..(23)
<223> Xaa at residue 1 is Gln or pyro-Glu

<400> 202
Xaa Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys Ala Cys
1 5 10 15

Lys Asn Leu Lys Cys Cys Ser
20

<210> 203
<211> 316
<212> DNA
<213> Conus stercusmuscarum

<400> 203
gatcgatagc agttcgtgat gtctaaactg ggagtcttgt tgaccatctg tctgcttctg 60

tttcccctta ctgctcttcc gatggatgga gatcaacctg cagaccaacc tgcagatcgt 120

atgcagaacg acatttcatc tgagcagtat cccttgtttg ataagagaca aaagtgttgc 180

ggccccggcg cgtcatgccc cagatatttc aaagacaatt ttatttgtgg ttgttgttaa 240

atgacaacgt gtcgatgacc aacttcgtta tcacgacttc gccaagtgtc taatgaataa 300

gtaaaacgat tgcagt 316
<210> 204
<211> 73
<212> PRT
<213> Conus stercusmuscarum

<400> 204
Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe Pro
1 5 10 15

Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro Ala
20 25 30

Asp Arg Met Gln Asn Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe Asp
35 40 45

Lys Arg Gln Lys Cys Cys Gly Pro Gly Ala Ser Cys Pro Arg Tyr Phe
50 55 60

Lys Asp Asn Phe Ile Cys Gly Cys Cys
65 70

<210> 205
<211> 23
<212> PRT
<213> Conus stercusmuscarum

<220>
<221> PEPTIDE
<222> (1)..(23)
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6 and 11 is P
ro or Hyp; Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-
iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 205
Xaa Lys Cys Cys Gly Xaa Gly Ala Ser Cys Xaa Arg Xaa Phe Lys Asp
1 5 10 15

Asn Phe Ile Cys Gly Cys Cys
20

<210> 206
<211> 331
<212> DNA
<213> Conus striatus

<400> 206
cgacctttca agagggatcg atagcagttc gcgatgtcta aactgggggt attgttgacc 60

atctgtctgc ttctgtttcc ccttactgct cttccgatgg atgaagatca acctgcagac 120

caacttgaag atcgtatgca ggacgacatt tcatctgagc agtatccctc gtttgttagg 180

agacaaaagt gttgcggcga aggctcgtca tgccccaaat atttcaaaaa caattttatt 240

tgtggttgtt gttaaatgac aacgtgtcga tgaccaactt cgttatcacg actacgccaa 300

gtgtcttgtc taatgataat aaaatgattc c 331

<210> 207
<211> 73
<212> PRT
<213> Conus striatus

<400> 207
Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe Pro
1 5 10 15

Leu Thr Ala Leu Pro Met Asp Glu Asp Gln Pro Ala Asp Gln Leu Glu
20 25 30

Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Ser Phe Val
35 40 45

Arg Arg Gln Lys Cys Cys Gly Glu Gly Ser Ser Cys Pro Lys Tyr Phe
50 55 60

Lys Asn Asn Phe Ile Cys Gly Cys Cys
65 70

<210> 208
<211> 23
<212> PRT
<213> Conus striatus

<220>
<221> PEPTIDE
<222> (1)..(23)
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6 is Glu or g
amma-carboxy Glu; Xaa at residue 11 is Pro or Hyp; Xaa at residue
13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or
O-phospho-Ty

<400> 208
Xaa Lys Cys Cys Gly Xaa Gly Ser Ser Cys Xaa Lys Xaa Phe Lys Asn
1 5 10 15

Asn Phe Ile Cys Gly Cys Cys
20

<210> 209
<211> 256
<212> DNA
<213> Conus striatus

<400> 209
ggatccatga tgtctaaact gggagtcttg ttgaccgtct gtctgcttct gtttcccctt 60

actgctcttc cgctggatgg agatcaacct gcagaccgac ctgcagagcg tatgcaggac 120

gacatttcat ctgacgagca tcccttgttt gataagagac aaaactgttg caatggggga 180

tgctccagca aatggtgcag agatcacgca cgttgttgcg gtcgatgata acgtgttgat 240

gaccaacttt ctcgag 256

<210> 210
<211> 75
<212> PRT

<213> Conus striatus

<400> 210
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Val Cys Leu Leu
1 5 10 15

Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp
20 25 30

Arg Pro Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Asp Glu His Pro
35 40 45

Leu Phe Asp Lys Arg Gln Asn Cys Cys Asn Gly Gly Cys Ser Ser Lys
50 55 60

Trp Cys Arg Asp His Ala Arg Cys Cys Gly Arg
65 70 75

<210> 211
<211> 20
<212> PRT
<213> Conus striatus

<220>
<221> PEPTIDE
<222> (1)..(20)
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 12 is Trp or bromo-Tr

<400> 211
Xaa Asn Cys Cys Asn Gly Gly Cys Ser Ser Lys Xaa Cys Arg Asp His
1 5 10 15

Ala Arg Cys Cys
20

<210> 212
<211> 235
<212> DNA
<213> Conus tessulatus

<400> 212
ggatccatga tgtctaaact gggagtcttg ttgaccatgt gtctgcttct gtttcccctt 60

actgctgttc cgctggatgg agatcaacct gcagaccgac ctgcagagcg taggcaggac 120

attgcaactg acgatcatcc tttgtttgat cccgtcaaac ggtgctgcca caaatgctat 180

atgggatgca tcccttgttg catttagtaa cgtgttgatg accaactttc tcgag 235

<210> 213
<211> 68
<212> PRT
<213> Conus tessulatus

<400> 213
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Met Cys Leu Leu
1 5 10 15

Leu Phe Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp
20 25 30

Arg Pro Ala Glu Arg Arg Gln Asp Ile Ala Thr Asp Asp His Pro Leu
35 40 45

Phe Asp Pro Val Lys Arg Cys Cys His Lys Cys Tyr Met Gly Cys Ile
50 55 60

Pro Cys Cys Ile
65

<210> 214
<211> 14
<212> PRT
<213> Conus tessulatus

<220>
<221> PEPTIDE
<222> (1)..(14)
<223> Xaa at residue 11 is Pro or Hyp; Xaa at residue 6 is Tyr, 125I-Ty
r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 214
Cys Cys His Lys Cys Xaa Met Gly Cys Ile Xaa Cys Cys Ile
1 5 10

<210> 215
<211> 238
<212> DNA
<213> Conus tessulatus

<400> 215
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtgtgcttct gtttcccctt 60

actgctgttc cgctggatgg agatcaacct gcagaccaac ctgcagagcg tacgcagaac 120

gagcagcatc ccttgtatga tcagaaaaga aagtgttgcc ggccgccatg cgccatgagc 180

tgcggcatgg ctaggtgttg ctattaatga taacgtgttg atgaccaact ttctcgag 238

<210> 216
<211> 68
<212> PRT
<213> Conus tessulatus

<400> 216
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Val Leu
1 5 10 15

Leu Phe Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp
20 25 30

Gln Pro Ala Glu Arg Thr Gln Asn Glu Gln His Pro Leu Tyr Asp Gln
35 40 45

Lys Arg Lys Cys Cys Arg Pro Pro Cys Ala Met Ser Cys Gly Met Ala
50 55 60

Arg Cys Cys Tyr
65

<210> 217
<211> 18
<212> PRT
<213> Conus tessulatus

<220>
<221> PEPTIDE
<222> (1)..(18)
<223> Xaa at residue 5 and 6 is Pro or Hyp; Xaa at residue 18 is Tyr, 1

25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 217
Lys Cys Cys Arg Xaa Xaa Cys Ala Met Ser Cys Gly Met Ala Arg Cys
1 5 10 15

Cys Xaa

<210> 218
<211> 564
<212> DNA
<213> Conus textile

<400> 218
gagtcaaccc actgtcacgc caagagcgga cgccacagct aaggcaagaa ggatcgatag 60

cagttcatga tgtctaaact gggagccttg ttgaccatct gtctacttct gttttccctt 120

actgctgttc cgctggatgg agatcaacat gcagaccaac ctgcacagcg tctgcaggac 180

cgcattccaa ctgaagatca tcccttattt gatcccaaca aacggtgttg cccgccggtg 240

gcatgcaaca tgggatgcaa gccttgttgt ggatgaccag ctttgttatc gcggtctcat 300

gaagtgtcta atgaataagt aaaacgattg cagtttcgtt cagatttgct gttgtatttt 360

ggtctaaaga ttaatgacca aactgttctt ttgatccgga ttttcacgta tttctcgatt 420

cctattcaac actagataag ttaatcacga cagatctgat tttccatcaa tgccttgctt 480

tttggtctgt catataaatc ttgtttatat ttaatttctc gtcactttca acacgcacac 540

acacacacac acacacgcgc gcgc 564

<210> 219
<211> 69
<212> PRT
<213> Conus textile

<400> 219
Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
20 25 30

Ala Gln Arg Leu Gln Asp Arg Ile Pro Thr Glu Asp His Pro Leu Phe
35 40 45

Asp Pro Asn Lys Arg Cys Cys Pro Pro Val Ala Cys Asn Met Gly Cys
50 55 60

Lys Pro Cys Cys Gly
65

<210> 220
<211> 16
<212> PRT
<213> Conus textile

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 3, 4 and 13 is Pro or Hyp

<400> 220
Cys Cys Xaa Xaa Val Ala Cys Asn Met Gly Cys Lys Xaa Cys Cys Gly
1 5 10 15

<210> 221
<211> 780
<212> DNA
<213> Conus textile

<400> 221
ggatccagac gacaaagaag agtcaaccca ctgccacgtc aagagcagag cccacagcta 60

agacaagaag gatcgatagc agttcatgat gtttaaactg ggagtcttgt tgaccatctg 120

tctccttctg ttttccctta atgctgttcc gttggatgga gatcaacctg cagaccaacc 180

tgcagagcgt ctgctggacg acatttcatt tgaaaataat cccttttatg atcccgccaa 240

acggtgttgc aggacttgct tcggttgcac accttgttgt ggatgaccag cctcatcaag 300

tgtctaacga ataagtaaag cgattgcagt ctcgttcaga tttacttttg tattctggtc 360

taaagattaa tgaccaaact cttcttttga tccggatgta catatatttc tcgattccta 420

tccaacgcta gataagctaa tcacgacaga tctgattttc tgtcaatgcc ttgctttttg 480

gtctctcata tcactcttgt ttatatttaa tttctcgtca ctatatatat atatacacac 540

acacacacac ggaattccga ttgtccagta ccgttcttgg gatcgaggta ttgctgcgat 600

ggcttattct gtactctttt cttctgcgct tgatagtgat gtcttctact cccatctgtg 660

ctacccctgg cttgatcttt gataggcgtg tgcccttcac tggttataaa cccctctgat 720

cctactctct ggacgcctcg ggggcccaac ctccaaataa agcgacatcc aatgaaaaaa 780

<210> 222
<211> 66
<212> PRT
<213> Conus textile

<400> 222
Met Met Phe Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Ser Leu Asn Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Pro
20 25 30

Ala Glu Arg Leu Leu Asp Asp Ile Ser Phe Glu Asn Asn Pro Phe Tyr
35 40 45

Asp Pro Ala Lys Arg Cys Cys Arg Thr Cys Phe Gly Cys Thr Pro Cys
50 55 60

Cys Gly
65

<210> 223
<211> 12
<212> PRT
<213> Conus textile

<220>
<221> PEPTIDE

<222> (1)..(12)
<223> Xaa at residue 10 is Pro or Hyp

<400> 223
Cys Cys Arg Thr Cys Phe Gly Cys Thr Xaa Cys Cys
1 5 10

<210> 224
<211> 456
<212> DNA
<213> Conus textile

<400> 224
ggaacagtca accccacagc cacgccaaga gcagacagcc acagctacgt gaagaagggt 60

ggagagaggt tcatgatgtt gaaaatggga gtggtgctat tcatctttct ggtactgttt 120

cccctggcaa cgctccagct ggatgcagat caacctgtag aacgatatgc ggagaacaaa 180

cagctcctca acccagatga aaggagggaa atcctattgc ctgctctgag gaagttctgc 240

tgtgattcga attggtgcca catttcggat tgtgagtgct gctacggtta gcgccgaaca 300

tccatggcac tgtgctgggc ggtttcatcc caacaacgac agcgtttgtt gatttcatgt 360

atcattgcgc ccacgtctct tgtctaagaa tgacgaacat gattgcactc tggttcagat 420

ttcgtgttct tttctgacaa taaatgacaa acctcc 456

<210> 225
<211> 70
<212> PRT
<213> Conus textile

<400> 225
Met Met Leu Lys Met Gly Val Val Leu Phe Ile Phe Leu Val Leu Phe
1 5 10 15

Pro Leu Ala Thr Leu Gln Leu Asp Ala Asp Gln Pro Val Glu Arg Tyr
20 25 30

Ala Glu Asn Lys Gln Leu Leu Asn Pro Asp Glu Arg Arg Glu Ile Leu
35 40 45

Leu Pro Ala Leu Arg Lys Phe Cys Cys Asp Ser Asn Trp Cys His Asp
50 55 60

Cys Glu Cys Cys Tyr Gly
65 70
<210> 226
<211> 17
<212> PRT
<213> Conus textile

<220>
<221> PEPTIDE
<222> (1)..(17)
<223> Xaa at residue 14 is Glu or gamma-carboxy Glu; Xaa at residue 7 i
s Trp or bromo-Trp; Xaa at residue 17 is Tyr, 125I-Tyr, mono-iodo
-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 226
Phe Cys Cys Asp Ser Asn Xaa Cys His Ile Ser Asp Cys Xaa Cys Cys
1 5 10 15

Xaa

<210> 227
<211> 456
<212> DNA
<213> Conus textile

<220>
<221> misc_feature
<222> (1)..(456)
<223> n may be any nucleotide

<400> 227
caaggaacag tcaaccccac agccacgcca agagcagaca gccacagcta cgtgaagaag 60

ggtggagaga ggttcgtgat gttgaaaatg ggagtggtgc tattcatctt cctggtactg 120

tttcccctgg caacgctcca gctggatgca gatcaacctg tagaacgata tgcggagaac 180

aaacagctcc tcagcccaga tgaaaggagg gaaatcatat tgcatgctct ggggacgcga 240

tgctgttctt gggatgtgtg cgaccacccg agttgtactt gctgcggtta gcgccgaaca 300

tccatggcgc tgtgctgggc ggttttatcc caacaacgac agcgtttgtt gatttcatgt 360

atcattgcgc ccacgtctct tgtctaagaa tgacgaacat gattgcactc tggttcagat 420

ttcgtgttct tttctgacaa taaatgacaa aacncc 456

<210> 228
<211> 70
<212> PRT
<213> Conus textile

<400> 228
Met Leu Lys Met Gly Val Val Leu Phe Ile Phe Leu Val Leu Phe Pro
1 5 10 15

Leu Ala Thr Leu Gln Leu Asp Ala Asp Gln Pro Val Glu Arg Tyr Ala
20 25 30

Glu Asn Lys Gln Leu Leu Ser Pro Asp Glu Arg Arg Glu Ile Ile Leu
35 40 45

His Ala Leu Gly Thr Arg Cys Cys Ser Trp Asp Val Cys Asp His Pro
50 55 60

Ser Cys Thr Cys Cys Gly
65 70

<210> 229
<211> 15
<212> PRT
<213> Conus textile

<220>
<221> PEPTIDE
<222> (1)..(15)
<223> Xaa at residue 10 is Pro or Hyp; Xaa at residue 4 is Trp or bromo
-Tr

<400> 229
Cys Cys Ser Xaa Asp Val Cys Asp His Xaa Ser Cys Thr Cys Cys
1 5 10 15

<210> 230
<211> 235
<212> DNA
<213> Conus textile

<400> 230
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt 60

actgctcttc cgctggatgg agatcaaccc gcagaccaag ctgcagagcg tatgcaggcc 120

gagcagcatc ccttgtttga tcagaaaaga cggtgctgca agtttccatg ccccgatagt 180

tgcagatatt tgtgttgcgg gtgatgataa cgtgttgatg accaactttc tcgag 235

<210> 231
<211> 67
<212> PRT
<213> Conus textile

<400> 231
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
1 5 10 15

Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp
20 25 30

Gln Ala Ala Glu Arg Met Gln Ala Glu Gln His Pro Leu Phe Asp Gln
35 40 45

Lys Arg Arg Cys Cys Lys Phe Pro Cys Pro Asp Ser Cys Arg Tyr Leu
50 55 60

Cys Cys Gly
65

<210> 232
<211> 16
<212> PRT
<213> Conus textile

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 3 and 8 is Pro or Hyp; Xaa at residue 13 is Tyr, 1
25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 232
Arg Cys Cys Lys Phe Xaa Cys Xaa Asp Ser Cys Arg Xaa Leu Cys Cys
1 5 10 15

<210> 233
<211> 321
<212> DNA
<213> Conus tulipa

<400> 233
cgacctcaag agggatcgat agcagttcat gtctaaactg ggagtcttgt tgacaatctg 60

tctgcttctg tttcccctta ctgctctgcc gatggatgga gatgaacctg cagaccgacc 120

tgcagagcgt atgcaggaca acatttcatc tgagcagcat cccttgtttg aggagagaca 180

cggatgttgc aaggggcccg aaggatgctc ctccagagaa tgcagacccc aacattgttg 240

cggtcgacga taacgtgttg agggccaact ttgttatcac ggctacgtca agtgtttagt 300

gaataagtaa aatgattgca g 321

<210> 234
<211> 74
<212> PRT
<213> Conus tulipa

<400> 234
Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe Pro
1 5 10 15

Leu Thr Ala Leu Pro Met Asp Gly Asp Glu Pro Ala Asp Arg Pro Ala
20 25 30

Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Leu Phe Glu
35 40 45

Glu Arg His Gly Cys Cys Lys Gly Pro Glu Gly Cys Ser Ser Arg Glu
50 55 60

Cys Arg Pro Gln His Cys Cys Gly Arg Arg
65 70

<210> 235
<211> 21
<212> PRT
<213> Conus tulipa

<220>
<221> PEPTIDE
<222> (1)..(21)
<223> Xaa at residue 8 and 14 is Glu or gamma-carboxy Glu; Xaa at resid
ue 7 and 17 is Pro or Hy

<400> 235
His Gly Cys Cys Lys Gly Xaa Xaa Gly Cys Ser Ser Arg Xaa Cys Arg
1 5 10 15

Xaa Gln His Cys Cys
20

<210> 236
<211> 287
<212> DNA
<213> Conus figulinus

<400> 236
caagaaggat cgatagcagt tcatgatgtc taaactggga gtcttgctga ccatctgtct 60

gcttctgatt ccccttactg ctctttcgct ggatggagat caacctgcag accgacctgc 120

agagcgtatg caggatggaa tttcatctga acagcatccc atgtttgatc ccgtcagacg 180

gtgttgcccg tggccatgca acataggatg cgtaccttgt tgttgatgac cagttttgtt 240

atcgcggcct catcaaatgt ctaatgaata agtaaaacga ttgcagt 287

<210> 237
<211> 67
<212> PRT
<213> Conus figulinus

<400> 237

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Ile
1 5 10 15

Pro Leu Thr Ala Leu Ser Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro
20 25 30

Ala Glu Arg Met Gln Asp Gly Ile Ser Ser Glu Gln His Pro Met Phe
35 40 45

Asp Pro Val Arg Arg Cys Cys Pro Trp Pro Cys Asn Ile Gly Cys Val
50 55 60

Pro Cys Cys
65

<210> 238
<211> 14
<212> PRT
<213> Conus figulinus

<220>
<221> PEPTIDE
<222> (1)..(14)
<223> Xaa at residue 3, 5 and 12 is Pro or Hyp; Xaa at residue 4 is Trp or bromo-Tr

<400> 238
Cys Cys Xaa Xaa Xaa Cys Asn Ile Gly Cys Val Xaa Cys Cys
1 5 10

<210> 239
<211> 283
<212> DNA
<213> Conus figulinus

<400> 239
caagagggat cgatagcagt tcatgatgtt taaactggga gtcctgttga ccatctgtat 60

gcttctgttt ccctttactg ctcttccgct ggatggagag caacctgcag accaacctgc 120

agagcgcatg cagtatgaca tgttacgtgc aatgaatccc tggtttgatc ccgtcaaaag 180

gtgctgctcg aagaactgcg cagtatgcat cccttgttgc ccgtaactga ccagcttgat 240

tatcgcggcc aaggctctaa tgaataagta aaacgattgc agt 283

<210> 240
<211> 67
<212> PRT
<213> Conus figulinus

<400> 240
Met Met Phe Lys Leu Gly Val Leu Leu Thr Ile Cys Met Leu Leu Phe
1 5 10 15

Pro Phe Thr Ala Leu Pro Leu Asp Gly Glu Gln Pro Ala Asp Gln Pro
20 25 30

Ala Glu Arg Met Gln Tyr Asp Met Leu Arg Ala Met Asn Pro Trp Phe
35 40 45

Asp Pro Val Lys Arg Cys Cys Ser Lys Asn Cys Ala Val Cys Ile Pro
50 55 60

Cys Cys Pro

65

<210> 241
<211> 14
<212> PRT
<213> Conus figulinus

<220>
<221> PEPTIDE
<222> (1)..(14)
<223> Xaa at residue 11 and 14 is Pro or Hyp

<400> 241
Cys Cys Ser Lys Asn Cys Ala Val Cys Ile Xaa Cys Cys Xaa
1 5 10

<210> 242
<211> 286
<212> DNA
<213> Conus figulinus

<400> 242
caagagggat cgatagcagt tcatgatgtc taaactgaga gtcttgttga ccttatgtct 60

gcttctgttt ccccttactg ctcttccgct gaatgaagat caacctgcag agcgtatgca 120

ggacgacaat tcatctgagc agcacccctt gtatgaccac aaacgaaagt gttgccggtg 180

gccatgcccc gcaagatgcg gctcttgttg cctgtaataa cgtgttggcc aactttgtta 240
tcacggccac gtcaaatgtt taatgaataa gtaaaacgat tgcagt 286

<210> 243
<211> 64
<212> PRT
<213> Conus figulinus

<400> 243
Met Met Ser Lys Leu Arg Val Leu Leu Thr Leu Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Leu Asn Glu Asp Gln Pro Ala Glu Arg Met
20 25 30

Gln Asp Asp Asn Ser Ser Glu Gln His Pro Leu Tyr Asp His Lys Arg
35 40 45

Lys Cys Cys Arg Trp Pro Cys Pro Ala Arg Cys Gly Ser Cys Cys Leu
50 55 60

<210> 244
<211> 15
<212> PRT
<213> Conus figulinus

<220>
<221> PEPTIDE
<222> (1)..(15)
<223> Xaa at residue 5 and 7 is Pro or Hyp; Xaa at residue 4 is Trp or bromo-Tr

<400> 244
Cys Cys Arg Xaa Xaa Cys Xaa Ala Arg Cys Gly Ser Cys Cys Leu
1 5 10 15

<210> 245

<211> 301
<212> DNA
<213> Conus figulinus

<400> 245
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccttatgtct 60

gcttctgttt cccctgactg ctcttccgct ggatgaagat caagctgcag accgacctgc 120

agagcgtatg cagggcatgt catctgaaca gcatcccttc tttgatcccg tcaaacggtg 180

ttgcgagttg tcacgctgcc ttggatgcgt cccttgttgc acatcttaat aacgtgtgga 240

tgaccaactg tgttatcacg gccacgtcaa gtgtctaatg aataagtaaa atgattgcag 300

t 301

<210> 246
<211> 68
<212> PRT
<213> Conus figulinus

<400> 246
Met Met Ser Lys Leu Gly Val Leu Leu Thr Leu Cys Leu Leu Leu Phe
1 5 10 15
Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Ala Ala Asp Arg Pro
20 25 30

Ala Glu Arg Met Gln Gly Met Ser Ser Glu Gln His Pro Phe Phe Asp
35 40 45

Pro Val Lys Arg Cys Cys Glu Leu Ser Arg Cys Leu Gly Cys Val Pro
50 55 60

Cys Cys Thr Ser
65

<210> 247
<211> 16
<212> PRT
<213> Conus figulinus

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 3 and 12 is Pro or Hyp

<400> 247
Cys Cys Xaa Leu Ser Arg Cys Leu Gly Cys Val Xaa Cys Cys Thr Ser
1 5 10 15

<210> 248
<211> 301
<212> DNA
<213> Conus figulinus

<400> 248
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccttatgtct 60

gcttctgttt cccctgactg ctcttccgct ggatgaagat caacctgcag accgacctgc 120

agagcgtatg cagggcatgt catctgaaca gcatcccttc tttgatcccg tcaaacggtg 180

ttgcgagttg tcaaaatgcc atggatgcgt cccttgttgc ataccttaat aacgtgcgga 240

tgaccaactg tgttatcacg gccacgtcaa gtgtctaatg aataagtaaa atgattgcag 300

t 301

<210> 249
<211> 68
<212> PRT
<213> Conus figulinus

<400> 249
Met Met Ser Lys Leu Gly Val Leu Leu Thr Leu Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Ala Asp Arg Pro
20 25 30

Ala Glu Arg Met Gln Gly Met Ser Ser Glu Gln His Pro Phe Phe Asp
35 40 45

Pro Val Lys Arg Cys Cys Glu Leu Ser Lys Cys His Gly Cys Val Pro
50 55 60
Cys Cys Ile Pro
65

<210> 250
<211> 16
<212> PRT
<213> Conus figulinus

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 12 a
nd 16 is Pro or Hy

<400> 250
Cys Cys Xaa Leu Ser Lys Cys His Gly Cys Val Xaa Cys Cys Ile Xaa
1 5 10 15

<210> 251
<211> 298
<212> DNA
<213> Conus quercinus

<400> 251
caagagggat cgatagcagt tcatgatgtc taaactcgga gtcttgttga ccatctgtct 60

ggttctgttt ccccttacag ctcttcagct ggatggagat caacctgcag accgacctgc 120

agagcgtacg caggacattt catctgaaca gtatcgaaag tttgatcaga gacagaggtg 180

ttgccggtgg ccatgccccg gtagttgcag atgctgccgt tatcgttaac gtgttggtga 240

ccagctttgt tatcacgacc acgccaagtg tctaacgaat aagtaaaatg attgcagt 298

<210> 252
<211> 68
<212> PRT
<213> Conus quercinus

<400> 252
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Val Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Gln Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro

20 25 30

Ala Glu Arg Thr Gln Asp Ile Ser Ser Glu Gln Tyr Arg Lys Phe Asp
35 40 45

Gln Arg Gln Arg Cys Cys Arg Trp Pro Cys Pro Gly Ser Cys Arg Cys
50 55 60

Cys Arg Tyr Arg
65

<210> 253
<211> 18
<212> PRT
<213> Conus quercinus

<220>
<221> PEPTIDE
<222> (1)..(18)
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 7 and 9 is Pr
o or Hyp; Xaa at residue 6 is Trp or bromo-Trp; Xaa at residue 17
is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-
phospho-Ty

<400> 253
Xaa Arg Cys Cys Arg Xaa Xaa Cys Xaa Gly Ser Cys Arg Cys Cys Arg
1 5 10 15

Xaa Arg

<210> 254
<211> 313
<212> DNA
<213> Conus quercinus

<400> 254
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct 60

gcttctgttt ccccttactg ctcttccact ggatggagat caacctgcag atcaatctgc 120

agagcgacct gcagagcgta cgcaggacga cattcagcag catccgttat atgatccgaa 180

aagaaggtgt tgccgttatc catgccccga cagctgccac ggatcttgct gctataagtg 240

ataacatgtt gatggccagc tttgttatca cggccacgtc aagtgtctaa tgaataagta 300

aaacgattgc agt 313

<210> 255
<211> 72
<212> PRT
<213> Conus quercinus

<400> 255
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Ser
20 25 30

Ala Glu Arg Pro Ala Glu Arg Thr Gln Asp Asp Ile Gln Gln His Pro
35 40 45

Leu Tyr Asp Pro Lys Arg Arg Cys Cys Arg Tyr Pro Cys Pro Asp Ser
50 55 60

Cys His Gly Ser Cys Cys Tyr Lys
65 70

<210> 256
<211> 18
<212> PRT
<213> Conus quercinus

<220>
<221> PEPTIDE
<222> (1)..(18)
<223> Xaa at residue 6 and 8 is Pro or Hyp; Xaa at residue 5 and 17 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phos pho-Ty

<400> 256
Arg Cys Cys Arg Xaa Xaa Cys Xaa Asp Ser Cys His Gly Ser Cys Cys
1 5 10 15

Xaa Lys

<210> 257
<211> 256
<212> DNA
<213> Conus wittigi

<400> 257
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccatt 60

actgctcttc cggtgggtgg agatcagcct gcagaccgac ttgcagagcg tatgcaggac 120

gacacttcat ctgagcagca tccctttgaa aagagactac catcatgttg cgactttgag 180

aggctttgcg tagtaccagc atgcatacgt catcagtgtt gcacaggata acgtgttgat 240

gaccaacttt ctcgag 256

<210> 258
<211> 74
<212> PRT
<213> Conus wittigi

<400> 258
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Ile Thr Ala Leu Pro Val Gly Gly Asp Gln Pro Ala Asp Arg Leu
20 25 30

Ala Glu Arg Met Gln Asp Asp Thr Ser Ser Glu Gln His Pro Phe Glu
35 40 45

Lys Arg Leu Pro Ser Cys Cys Asp Phe Glu Arg Leu Cys Val Val Pro
50 55 60

Ala Cys Ile Arg His Gln Cys Cys Thr Gly
65 70

<210> 259
<211> 23
<212> PRT
<213> Conus wittigi

<220>

<221> PEPTIDE
<222> (1)..(23)
<223> Xaa at residue 8 is Glu or gamma-carboxy Glu; Xaa at residue 2 an
d 14 is Pro or Hy

<400> 259
Leu Xaa Ser Cys Cys Asp Phe Xaa Arg Leu Cys Val Val Xaa Ala Cys
1 5 10 15

Ile Arg His Gln Cys Cys Thr
20

<210> 260
<211> 14
<212> PRT
<213> Conus betulinus

<220>
<221> PEPTIDE
<222> (1)..(14)
<223> Xaa at residue 11 is Pro or Hyp; Xaa at residue 14 is Trp or brom
o-Tr

<400> 260
Cys Cys Lys Gln Ser Cys Thr Thr Cys Met Xaa Cys Cys Xaa
1 5 10

<210> 261
<211> 259
<212> DNA
<213> Conus tulipa

<220>
<221> misc_feature
<222> (1)..(259)
<223> n may be any nucleotide

<400> 261
ggatccatga tgtctaaact gggagtcttg ttgacaatct gtctgcttct gtttcccctt 60

actgctctgc cgatggatgg agatgaacct gcagaccgac ctgcagagcg tatgcaggac 120

aacatttcat ctgagcagca tcccttgttt gaggagagac acggatgttg cgaggggccg 180

aagggatgct cctccagaga atgcagaccc caacattgtt gcggtcgacg ataacgtgtt 240

gatgaccaac tntctcgag 259

<210> 262
<211> 75
<212> PRT
<213> Conus tulipa

<400> 262
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Glu Pro Ala Asp Arg Pro
20 25 30

Ala Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Leu Phe
35 40 45

Glu Glu Arg His Gly Cys Cys Glu Gly Pro Lys Gly Cys Ser Ser Arg
50 55 60

Glu Cys Arg Pro Gln His Cys Cys Gly Arg Arg
65 70 75

<210> 263
<211> 21
<212> PRT
<213> Conus tulipa

<220>
<221> PEPTIDE
<222> (1)..(21)
<223> Xaa at residue 5 and 14 is Glu or gamma-carboxy Glu; Xaa at resid
ue 7 and 17 is Pro or Hy

<400> 263
His Gly Cys Cys Xaa Gly Xaa Lys Gly Cys Ser Ser Arg Xaa Cys Arg
1 5 10 15

Xaa Gln His Cys Cys
20

<210> 264
<211> 262
<212> DNA
<213> Conus aurisiacus

<220>
<221> misc_feature
<222> (1)..(262)
<223> n may be any nucleotide

<400> 264
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctacttct gtttcccctt 60

actgcttttc cgatggatgg agatcaacct gcagaccaac ctgcagatcg tatgcaggac 120

gacatttcat ctgagcagta tcccttgttt gataagagac aaaagtgttg cactgggagg 180

aaggggtcat gctccggcaa agcatgcaaa aatctcaaat gttgctctgg acgataacgt 240

gttgatgacc aactttctcg an 262

<210> 265
<211> 76
<212> PRT
<213> Conus aurisiacus

<400> 265
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Phe Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro
20 25 30

Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe
35 40 45

Asp Lys Arg Gln Lys Cys Cys Thr Gly Arg Lys Gly Ser Cys Ser Gly
50 55 60

Lys Ala Cys Lys Asn Leu Lys Cys Cys Ser Gly Arg
65 70 75

<210> 266

<211> 23
<212> PRT
<213> Conus aurisiacus

<220>
<221> PEPTIDE
<222> (1)..(23)
<223> Xaa at residue 1 is Gln or pyro-Glu

<400> 266
Xaa Lys Cys Cys Thr Gly Arg Lys Gly Ser Cys Ser Gly Lys Ala Cys
1 5 10 15

Lys Asn Leu Lys Cys Cys Ser
20

<210> 267
<211> 239
<212> DNA
<213> Conus betulinus

<400> 267
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt 60

actgctgttc cgttggatgg agatcaacct gcagaccaac ctgcagagcg tatgcagaac 120

gagcagcatc cctcgtttga tcagaaaaga aggtgctgcc ggtggccatg ccccagtata 180

tgcggcatgg ctaggtgttg cttcgtcatg ataacgtgtt gatgaccaac tttctcgag 239

<210> 268
<211> 71
<212> PRT
<213> Conus betulinus

<400> 268
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Pro
20 25 30

Ala Glu Arg Met Gln Asn Glu Gln His Pro Ser Phe Asp Gln Lys Arg
35 40 45

Arg Cys Cys Arg Trp Pro Cys Pro Ser Ile Cys Gly Met Ala Arg Cys
50 55 60

Cys Phe Val Met Ile Thr Cys
65 70

<210> 269
<211> 23
<212> PRT
<213> Conus betulinus

<220>
<221> PEPTIDE
<222> (1)..(23)
<223> Xaa at residue 6 and 8 is Pro or Hyp; Xaa at residue 5 is Trp or bromo-Tr

<400> 269
Arg Cys Cys Arg Xaa Xaa Cys Xaa Ser Ile Cys Gly Met Ala Arg Cys
1 5 10 15

Cys Phe Val Met Ile Thr Cys
20

<210> 270
<211> 226
<212> DNA
<213> Conus betulinus

<220>
<221> misc_feature
<222> (1)..(226)
<223> n may be any nucleotide

<400> 270
ggatccatga tgtctaaact gggagtcttg ttgatcatct gtctgcttct gtttcccctt 60

actgctgttc cgctggatgg agatcagcct gcagagcgta cgcagatcga gcagcatccc 120

ttgtttgacc agaaaagaag gtgttgccgg tggccatgcc ccagtagatg cggcatggct 180

aggtgttgct tcgtcatgat aacgtgttga tgancgacct ctcnag 226

<210> 271
<211> 67
<212> PRT
<213> Conus betulinus

<400> 271
Met Met Ser Lys Leu Gly Val Leu Leu Ile Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Glu Arg Thr
20 25 30

Gln Ile Glu Gln His Pro Leu Phe Asp Gln Lys Arg Arg Cys Cys Arg
35 40 45

Trp Pro Cys Pro Ser Arg Cys Gly Met Ala Arg Cys Cys Phe Val Met
50 55 60

Ile Thr Cys
65

<210> 272
<211> 23
<212> PRT
<213> Conus betulinus

<220>
<221> PEPTIDE
<222> (1)..(23)
<223> Xaa at residue 6 and 8 is Pro or Hyp; Xaa at residue 5 is Trp or bromo-Tr

<400> 272
Arg Cys Cys Arg Xaa Xaa Cys Xaa Ser Arg Cys Gly Met Ala Arg Cys
1 5 10 15
Cys Phe Val Met Ile Thr Cys
20

<210> 273
<211> 262
<212> DNA
<213> Conus parius

<400> 273
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt 60

actgctcttc cgatggatgg tgatcaacct gcagaccgac ttgtagagcg tatgcaggac 120

aacatttcat ctgagcagca tcccttcttt gaaaagagaa gaggaggctg ttgcacacct 180

ccgaagaaat gcaaagaccg agcctgcaaa cctgcacgtt gctgcggccc aggataacgt 240

gttgatgacc aactttctcg cc 262

<210> 274
<211> 76
<212> PRT
<213> Conus parius

<400> 274
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Leu
20 25 30

Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe
35 40 45

Glu Lys Arg Arg Gly Gly Cys Cys Thr Pro Pro Lys Lys Cys Lys Asp
50 55 60

Arg Ala Cys Lys Pro Ala Arg Cys Cys Gly Pro Gly
65 70 75

<210> 275
<211> 24
<212> PRT
<213> Conus parius

<220>
<221> PEPTIDE
<222> (1)..(24)
<223> Xaa at residue 7, 8, 18 and 24 is Pro or Hyp

<400> 275
Arg Gly Gly Cys Cys Thr Xaa Xaa Lys Lys Cys Lys Asp Arg Ala Cys
1 5 10 15

Lys Xaa Ala Arg Cys Cys Gly Xaa
20

<210> 276
<211> 259
<212> DNA
<213> Conus parius
<400> 276
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt 60

actgctcttc cgatggatgg tgatcaacct gcagaccgac ttgtagagcg tatgcaggac 120

aacatttcat ctgagcagca tcccttcttt gaaaagagaa gaggctgttg cacacctccg 180

aggaaatgca aagaccgagc ctgcaaacct gcacgttgtt gcggcccagg ataacgtgtt 240

gatgaccaac tttctcgag 259

<210> 277
<211> 75
<212> PRT
<213> Conus parius

<400> 277
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Leu
20 25 30

Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe
35 40 45

Glu Lys Arg Arg Gly Cys Cys Thr Pro Pro Arg Lys Cys Lys Asp Arg
50 55 60

Ala Cys Lys Pro Ala Arg Cys Cys Gly Pro Gly
65 70 75

<210> 278
<211> 23
<212> PRT
<213> Conus parius

<220>
<221> PEPTIDE
<222> (1)..(23)
<223> Xaa at residue 6, 7, 17 and 23 is Pro or Hyp

<400> 278
Arg Gly Cys Cys Thr Xaa Xaa Arg Lys Cys Lys Asp Arg Ala Cys Lys
1 5 10 15

Xaa Ala Arg Cys Cys Gly Xaa
20

<210> 279
<211> 241
<212> DNA
<213> Conus coronatus

<400> 279
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttccaatt 60

actgcccttc cgctggatga agatcaacct gcagaccgac ctgcagagcg tatgcaggac 120

attgcaactg aacagcatcc cttgtttgat cccgtcaaac ggtgctgcga ttggccatgc 180

atcccaggat gcaccccttg ttgcttgcct tgataacgtg ttgatgacca actttctcga 240

g 241

<210> 280
<211> 68
<212> PRT
<213> Conus coronatus

<400> 280
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Ile Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Ala Asp Arg Pro
20 25 30

Ala Glu Arg Met Gln Asp Ile Ala Thr Glu Gln His Pro Leu Phe Asp
        35   40   45

Pro Val Lys Arg Cys Cys Asp Trp Pro Cys Ile Pro Gly Cys Thr Pro
    50   55   60

Cys Cys Leu Pro
65

<210> 281
<211> 16
<212> PRT
<213> Conus coronatus

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 5, 8, 12 and 16 is Pro or Hyp; Xaa at residue 4 is Trp or bromo-Tr

<400> 281
Cys Cys Asp Xaa Xaa Cys Ile Xaa Gly Cys Thr Xaa Cys Cys Leu Xaa
1   5   10   15

<210> 282
<211> 244
<212> DNA
<213> Conus musicus

<400> 282
ggatccatga tgtctaaact gggagtcctg ttgaccatct gtctgcttct gtttcctctt 60

tctgctcttc cgatggatga agatcaactt gcagacctac ctgcagagcg tatgcgggac 120

actgcaactg tagatcatcc ctcctatgat cctgacaaag cgtgctgcga gcagagctgt 180

acaacatgct ttccgtgctg ctagccttga acacagtaac gtgttgatga ccaactttct 240

cgag 244

<210> 283
<211> 65
<212> PRT
<213> Conus musicus

<400> 283
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1   5   10   15

Pro Leu Ser Ala Leu Pro Met Asp Glu Asp Gln Leu Ala Asp Leu Pro
            20   25   30

Ala Glu Arg Met Arg Asp Thr Ala Thr Val Asp His Pro Ser Tyr Asp
        35   40   45

Pro Asp Lys Ala Cys Cys Glu Gln Ser Cys Thr Thr Cys Phe Pro Cys
    50   55   60

Cys
65

<210> 284
<211> 14
<212> PRT

<213> Conus musicus

<220>
<221> PEPTIDE
<222> (1)..(14)
<223> Xaa at residue4 is Glu or gamma-carboxy Glu; Xaa at residue 12 i
s Pro or Hy

<400> 284
Ala Cys Cys Xaa Gln Ser Cys Thr Thr Cys Phe Xaa Cys Cys
1 5 10

<210> 285
<211> 14
<212> PRT
<213> Conus betulinus

<220>
<221> PEPTIDE
<222> (1)..(14)
<223> Xaa at residue 4 is Glu or gamma-carboxy Glu; Xaa at residue 12 i
s Pro or Hy

<400> 285
Ala Cys Cys Xaa Gln Ser Cys Thr Thr Cys Met Xaa Cys Cys
1 5 10

<210> 286
<211> 14
<212> PRT
<213> Conus betulinus

<220>
<221> PEPTIDE
<222> (1)..(14)
<223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 11 i
s Pro or Hyp; Xaa at residue 14 is Trp or bromo-Tr

<400> 286
Cys Cys Xaa Gln Ser Cys Thr Thr Cys Met Xaa Cys Cys Xaa
1 5 10

<210> 287
<211> 235
<212> DNA
<213> Conus pennaceus

<400> 287
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt 60

actgctcttc cgctggatgg agatcaacct gcataccaag ctgcagagcg tatgcaggcc 120

gagcatcatc ccttgtttga tcagaaaaga cggtgctgca agtttccatg ccccgatagt 180

tgcaaatatt tgtgttgcgg gtgatgataa catgttgatg accaactttc ttgag 235

<210> 288
<211> 65
<212> PRT
<213> Conus pennaceus

<400> 288
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

```
Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Tyr Gln Ala
            20                  25                  30

Ala Glu Arg Met Gln Ala Glu His His Pro Leu Phe Asp Gln Lys Arg
        35                  40                  45

Arg Cys Cys Lys Phe Pro Cys Pro Asp Ser Cys Lys Tyr Leu Cys Cys
    50                  55                  60

Gly
65

&lt;210&gt;  289
&lt;211&gt;  16
&lt;212&gt;  PRT
&lt;213&gt;  Conus pennaceus

&lt;220&gt;
&lt;221&gt;  PEPTIDE
&lt;222&gt;  (1)..(16)
&lt;223&gt;  Xaa at residue 6 and 8 is Pro or Hyp; Xaa at residue 13 is Tyr, 1
       25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty


&lt;400&gt;  289
Arg Cys Cys Lys Phe Xaa Cys Xaa Asp Ser Cys Lys Xaa Leu Cys Cys
1               5                   10                  15

&lt;210&gt;  290
&lt;211&gt;  241
&lt;212&gt;  DNA
&lt;213&gt;  Conus pulicarius

&lt;400&gt;  290
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt      60

actgctcttc cgatggatgg tgatcaactt gcagaccgac ttgtagagcg tatgcaggac     120

aacatttcat ctgagcagca tcccttcttt gatcccgtca aacggtgttg cgtcagctgt     180

tacatgggat gcatcccttg ttgcttctag taataacgtg ttgatgacca actttctcga     240

g                                                                     241

&lt;210&gt;  291
&lt;211&gt;  67
&lt;212&gt;  PRT
&lt;213&gt;  Conus pulicarius

&lt;400&gt;  291
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1               5                   10                  15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Leu Ala Asp Arg Leu
            20                  25                  30

Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe
        35                  40                  45

Asp Pro Val Lys Arg Cys Cys Val Ser Cys Tyr Met Gly Cys Ile Pro
    50                  55                  60

Cys Cys Phe
65
```

<210> 292
<211> 14
<212> PRT
<213> Conus pulicarius

<220>
<221> PEPTIDE
<222> (1)..(14)
<223> Xaa at residue 11 is Pro or Hyp; Xaa at residue 6 is Tyr, 125I-Ty
r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 292
Cys Cys Val Ser Cys Xaa Met Gly Cys Ile Xaa Cys Cys Phe
1 5 10

<210> 293
<211> 244
<212> DNA
<213> Conus pulicarius

<400> 293
ggatccatga tgtctaaact gggagtcttg ttgaccgtct gtctgcttct gtgtcccctt 60

actgctcttc cactggatga agatcaactt gcagaccgac ctgcagagcg tatgcaggat 120

gacacttcag ctgcacagat tttcgggttt gatcccgtca aacggtgctg caaattgcta 180

tgctactcgg gatgcactcc ttgttgccat atttgataac gtgttgatga ccaactttct 240

cgag 244

<210> 294
<211> 67
<212> PRT
<213> Conus pulicarius

<400> 294
Met Met Ser Lys Leu Gly Val Leu Leu Thr Val Cys Leu Leu Leu Cys
1 5 10 15

Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Leu Ala Asp Arg Pro
20 25 30

Ala Glu Arg Met Gln Asp Asp Thr Ser Ala Ala Gln Ile Phe Gly Phe
35 40 45

Asp Pro Val Lys Arg Cys Cys Lys Leu Leu Cys Gly Cys Thr Pro Cys
50 55 60

Cys His Ile
65

<210> 295
<211> 16
<212> PRT
<213> Conus pulicarius

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 12 is Pro or Hyp; Xaa at residue 7 is Tyr, 125I-Ty
r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 295
Cys Cys Lys Leu Leu Cys Xaa Ser Gly Cys Thr Xaa Cys Cys His Ile

1 5 10 15

<210> 296
<211> 259
<212> DNA
<213> Conus rattus

<400> 296
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttgt gtttccgctt 60

actgctcttc cgatggatgg tgatcaacct gcagaccgac ttgtagagcg tatacaggac 120

aacatttcat ctgagcagca tcccttcttt gaaaagagaa gaggctgttg cgcacctccg 180

aggaaatgca aagaccgagc ctgcaaacct gcacgttgct gcggcccagg ataacgtgtt 240

gatgaccaac tttctcgag 259

<210> 297
<211> 75
<212> PRT
<213> Conus rattus

<400> 297
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Val Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Leu
20 25 30

Val Glu Arg Ile Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe
35 40 45

Glu Lys Arg Arg Gly Cys Cys Ala Pro Pro Arg Lys Cys Lys Asp Arg
50 55 60

Ala Cys Lys Pro Ala Arg Cys Cys Gly Pro Gly
65 70 75

<210> 298
<211> 23
<212> PRT
<213> Conus rattus

<220>
<221> PEPTIDE
<222> (1)..(23)
<223> Xaa at residue 6, 7, 17 and 23 is Pro or Hyp

<400> 298
Arg Gly Cys Cys Ala Xaa Xaa Arg Lys Cys Lys Asp Arg Ala Cys Lys
1 5 10 15

Xaa Ala Arg Cys Cys Gly Xaa
20

<210> 299
<211> 262
<212> DNA
<213> Conus stercusmuscarum

<400> 299
ggatccatga tgtctaaact gggagtcttg ttgacaatct gtctgcttct gtttcccctt 60

attgctcttc cgctggatgg agatcaacct gcagaccgac ctgcagagcg tatgcaggac 120

gacatttcat ctgagaagca tcccttgttt gataagagac aacggtgttg caatgggcgg 180

aggggatgct ccagcagatg gtgcagagat cactcacgtt gttgcggtcg acgataacgt 240

gttgatgacc aactttctcg ag 262

<210> 300
<211> 76
<212> PRT
<213> Conus stercusmuscarum

<400> 300
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Ile Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro
20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Lys His Pro Leu Phe
35 40 45

Asp Lys Arg Gln Arg Cys Cys Asn Gly Arg Arg Gly Cys Ser Ser Arg
50 55 60

Trp Cys Arg Asp His Ser Arg Cys Cys Gly Arg Arg
65 70 75

<210> 301
<211> 22
<212> PRT
<213> Conus stercusmuscarum

<220>
<221> PEPTIDE
<222> (1)..(22)
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 14 is Trp or bromo-Tr

<400> 301
Xaa Arg Cys Cys Asn Gly Arg Arg Gly Cys Ser Ser Arg Xaa Cys Arg
1 5 10 15

Asp His Ser Arg Cys Cys
20

<210> 302
<211> 241
<212> DNA
<213> Conus ebraceus

<400> 302
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt 60

actgctcttc cactggatga aggtcaacct gcagacctac ctgcagagcg tatgcaggac 120

attgcaactg aacagcatcc cttgtttgat cctgtcaaac ggtgttgcga gcagccatgc 180

tacatgggat gcatcccttg ttgcttctaa taataacgtg ttgatgacca actttctcga 240

g 241

<210> 303
<211> 67
<212> PRT

<213> Conus ebraceus

<400> 303
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Leu Asp Glu Gly Gln Pro Ala Asp Leu Pro
20 25 30

Ala Glu Arg Met Gln Asp Ile Ala Thr Glu Gln His Pro Leu Phe Asp
35 40 45

Pro Val Lys Arg Cys Cys Glu Gln Pro Cys Tyr Met Gly Cys Ile Pro
50 55 60

Cys Cys Phe
65

<210> 304
<211> 15
<212> PRT
<213> Conus ebraceus
<220>
<221> PEPTIDE
<222> (1)..(15)
<223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 5 an
d 12 is Pro or Hyp; Xaa at residue 7 is Tyr, 125I-Tyr, mono-iodo-
Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 304
Cys Cys Xaa Gln Xaa Cys Xaa Met Gly Cys Ile Xaa Cys Cys Phe
1 5 10 15

<210> 305
<211> 241
<212> DNA
<213> Conus ebraceus

<400> 305
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt 60

actgctcttc cactggatga agatcaacct gcagacctac ctgcagagcg tatgcaggac 120

attgcaactg aacagcatcc cttgtttgat cctgtcaaac ggtgctgcgc gcagccatgc 180

tacatgggat gcatcccttg ttgcttctaa taataacgtg ttgatgacca actttctcga 240

g 241

<210> 306
<211> 67
<212> PRT
<213> Conus ebraceus

<400> 306
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Ala Asp Leu Pro
20 25 30

Ala Glu Arg Met Gln Asp Ile Ala Thr Glu Gln His Pro Leu Phe Asp
35 40 45

Pro Val Lys Arg Cys Cys Ala Gln Pro Cys Tyr Met Gly Cys Ile Pro

50 55 60

Cys Cys Phe
65

<210> 307
<211> 15
<212> PRT
<213> Conus ebraceus

<220>
<221> PEPTIDE
<222> (1)..(15)
<223> Xaa at residue 5 and 12 is Pro or Hyp; Xaa at residue 7 is Tyr, 1
25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 307
Cys Cys Ala Gln Xaa Cys Xaa Met Gly Cys Ile Xaa Cys Cys Phe
1 5 10 15

<210> 308
<211> 238
<212> DNA
<213> Conus flavidus

<400> 308
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt 60

actgctgttc cgttggatgg agatcaacct gcagaccagc ctgcagagcg tatgcagaac 120

gagcagcatc ccttgtttga tcagaaaaga aggtgctgcc ggtggccatg ccccagtata 180

tgcggcatgg ctaggtgttg ctcgtcatga taacgtgttg atgaccaact ttctcgag 238

<210> 309
<211> 67
<212> PRT
<213> Conus flavidus

<400> 309
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Pro
20 25 30

Ala Glu Arg Met Gln Asn Glu Gln His Pro Leu Phe Asp Gln Lys Arg
35 40 45

Arg Cys Cys Arg Trp Pro Cys Pro Ser Ile Cys Gly Met Ala Arg Cys
50 55 60

Cys Ser Ser
65

<210> 310
<211> 19
<212> PRT
<213> Conus flavidus

<220>
<221> PEPTIDE
<222> (1)..(19)
<223> Xaa at residue 6 and 8 is Pro or Hyp; Xaa at residue 5 is Trp or

bromo-Tr

<400> 310
Arg Cys Cys Arg Xaa Xaa Cys Xaa Ser Ile Cys Gly Met Ala Arg Cys
1 5 10 15

Cys Ser Ser

<210> 311
<211> 245
<212> DNA
<213> Conus miliaris

<220>
<221> misc_feature
<222> (1)..(245)
<223> n may be any nucleotide

<400> 311
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttccaatt 60

actgcccttc cactggatga agatcaacct gcagaccgac ctgcagagcg tatgcaggac 120

attgcaactg aacagcatcc cttgtttgat cccgtcaaac ggtgttgcga ttggccatgc 180

agcgcaggat gctacccttg ttgcttccct taataacgtg ttgatgacca actnangnaa 240

aaaaa 245

<210> 312
<211> 68
<212> PRT
<213> Conus miliaris

<400> 312
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Ile Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Ala Asp Arg Pro
20 25 30

Ala Glu Arg Met Gln Asp Ile Ala Thr Glu Gln His Pro Leu Phe Asp
35 40 45

Pro Val Lys Arg Cys Cys Asp Trp Pro Cys Ser Ala Gly Cys Tyr Pro
50 55 60

Cys Cys Phe Pro
65

<210> 313
<211> 16
<212> PRT
<213> Conus miliaris

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 5, 12 and 16 is Pro or Hyp; Xaa at residue 4 is Tr
p or bromo-Trp; Xaa at residue 11 is Tyr, 125I-Tyr, mono-iodo-Tyr
, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 313
Cys Cys Asp Xaa Xaa Cys Ser Ala Gly Cys Xaa Xaa Cys Cys Phe Xaa
1 5 10 15

<210> 314
<211> 230
<212> DNA
<213> Conus miliaris

<220>
<221> misc_feature
<222> (1)..(230)
<223> n may be any nucleotide
<400> 314
ggatccatga tgtctaaact gggagtggtg ccattcgtct ttctggtcct gtttcccctg 60

gcaacactcc aactggatgc agatcaacct gcagaccgac ctgcgcgtaa aaagggcatt 120

gcaactaaac ggcatccctt gtctgatcct gtcagagggt gttgccctcc aatgtgcaca 180

ccatgcttcc cttgctgttt tcgttaataa cgtgttgatg natgatgnan 230

<210> 315
<211> 66
<212> PRT
<213> Conus miliaris

<400> 315
Met Met Ser Lys Leu Gly Val Val Pro Phe Val Phe Leu Val Leu Phe
1 5 10 15

Pro Leu Ala Thr Leu Gln Leu Asp Ala Asp Gln Pro Ala Asp Arg Pro
20 25 30

Ala Arg Lys Lys Gly Ile Ala Thr Lys Arg His Pro Leu Ser Asp Pro
35 40 45

Val Arg Gly Cys Cys Pro Pro Met Cys Thr Pro Cys Phe Pro Cys Cys
50 55 60

Phe Arg
65

<210> 316
<211> 16
<212> PRT
<213> Conus miliaris

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 4, 9 and 12 is Pro or Hyp; Xaa at residue 5 is Tyr
, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho
-Ty

<400> 316
Gly Cys Cys Xaa Xaa Met Cys Thr Xaa Cys Phe Xaa Cys Cys Phe Arg
1 5 10 15

<210> 317
<211> 295
<212> DNA
<213> Conus ammiralis

<400> 317
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct 60

gcttctgttt ccccttactg ctcttccgct ggatggagat caacctgcag accaagctgc 120

```
agagcgtatg caggccgagc agcatccctt gtttgatcag aaaagacggt gttgcaggtt     180

tccatgcccc gatacttgca gacatttgtg ttgcgggtga tgataacgtg ctgatgaccc     240

actttgtcat cacggctacg tcaagtgtct aatgaataag taaaatgatt gcagt         295
<210>  318
<211>  65
<212>  PRT
<213>  Conus ammiralis

<400>  318
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1               5                   10                  15

Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Ala
            20                  25                  30

Ala Glu Arg Met Gln Ala Glu Gln His Pro Leu Phe Asp Gln Lys Arg
        35                  40                  45

Arg Cys Cys Arg Phe Pro Cys Pro Asp Thr Cys Arg His Leu Cys Cys
    50                  55                  60

Gly
65

<210>  319
<211>  16
<212>  PRT
<213>  Conus ammiralis

<220>
<221>  PEPTIDE
<222>  (1)..(16)
<223>  Xaa at residue 6 and 8 is Pro or Hyp

<400>  319
Arg Cys Cys Arg Phe Xaa Cys Xaa Asp Thr Cys Arg His Leu Cys Cys
1               5                   10                  15

<210>  320
<211>  267
<212>  DNA
<213>  Conus ammiralis

<400>  320
caagagggat cgatagcagt tcatgatgtt taaactggga gtcttgctga ccatctgtct      60

acttctgttt tcccttaatg ctgttccgct ggatggagat caacctgcag accaacctgc     120

agagcgtctg ctggacgaca tttcatctga aaataatccc ttttatgatc ccgccaaacg     180

gtgttgcatg acttgcttcg gttgcacacc ttgttgtgga tgaccagcct catcaagtgt     240

ctaacgaata agtaaaacga ttgcagt                                         267

<210>  321
<211>  66
<212>  PRT
<213>  Conus ammiralis

<400>  321
Met Met Phe Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1               5                   10                  15
```

Ser Leu Asn Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Pro
20 25 30

Ala Glu Arg Leu Leu Asp Asp Ile Ser Ser Glu Asn Asn Pro Phe Tyr
35 40 45

Asp Pro Ala Lys Arg Cys Cys Met Thr Cys Phe Gly Cys Thr Pro Cys
50 55 60

Cys Gly
65

<210> 322
<211> 12
<212> PRT
<213> Conus ammiralis

<220>
<221> PEPTIDE
<222> (1)..(12)
<223> Xaa at residue 10 is Pro or Hyp

<400> 322
Cys Cys Met Thr Cys Phe Gly Cys Thr Xaa Cys Cys
1 5 10

<210> 323
<211> 294
<212> DNA
<213> Conus ammiralis

<400> 323
caagaaggat cgatagcagt tcatgatgtc taaactggga gccttgttga ccatctgtct 60

acttctgttt tcccttactg ctgttccgct ggatggagat caacatgcag accaacctgc 120

agagcgtctg caggaccgcc ttccaactga aaatcatccc ttatatgatc ccgtcaaacg 180

gtgttgcgat gattcggaat gcgactattc ttgctggcct tgctgtattt tttcataacc 240

tttgttatcg cggcctcatc ctagtgtcaa atgaataagt aaaacgattg cagt 294

<210> 324
<211> 71
<212> PRT
<213> Conus ammiralis

<400> 324
Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
20 25 30

Ala Glu Arg Leu Gln Asp Arg Leu Pro Thr Glu Asn His Pro Leu Tyr
35 40 45

Asp Pro Val Lys Arg Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys
50 55 60

Trp Pro Cys Cys Ile Phe Ser
65 70
<210> 325
<211> 18

<212> PRT
<213> Conus ammiralis

<220>
<221> PEPTIDE
<222> (1)..(18)
<223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 i s Pro or Hyp; Xaa at residue 12 is Trp or bromo-Trp; Xaa at resid ue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr o r O-phospho-Ty

<400> 325
Cys Cys Asp Asp Ser Xaa Cys Asp Xaa Ser Cys Xaa Xaa Cys Cys Ile
1 5 10 15

Phe Ser

<210> 326
<211> 284
<212> DNA
<213> Conus ammiralis

<400> 326
caagagggat cgatagcagt tcatgatgtt taaactcgga gtcttgctga ccatctgtct 60

acttctgttt tccctaattg ctgttccgct ggatggagat caacatgcag accaacctgc 120

agagcgtctg caggaccgcc ttccaactga aaatcatccc ttatatgatc ccgtcaaacg 180

gtgttgcagg ttgttatgcc tcagttgcaa cccttgttgt ggatgaccag ctttgttatc 240

acggcctcat caagtgtcta atgaataagt aaaacgattg cagt 284

<210> 327
<211> 67
<212> PRT
<213> Conus ammiralis

<400> 327
Met Met Phe Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Ser Leu Ile Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
20 25 30

Ala Glu Arg Leu Gln Asp Arg Leu Pro Thr Glu Asn His Pro Leu Tyr
35 40 45

Asp Pro Val Lys Arg Cys Cys Arg Leu Leu Cys Leu Ser Cys Asn Pro
50 55 60

Cys Cys Gly
65

<210> 328
<211> 13
<212> PRT
<213> Conus ammiralis

<220>
<221> PEPTIDE
<222> (1)..(13)
<223> Xaa at residue 11 is Pro or Hyp

<400> 328

Cys Cys Arg Leu Leu Cys Leu Ser Cys Asn Xaa Cys Cys
1 5 10

<210> 329
<211> 289
<212> DNA
<213> Conus ammiralis

<400> 329
caagaaggat cgatagcagt tcatgatgtc taaactggga gccttgttga ccatctgtct 60

acttctgttt tcccttactg ctgttccgct ggatggagat caacatgcag accaacctgc 120

agagcgtctg caggaccgca ttccaactga agatcatccc ttatttgatc ccaacaaacg 180

gtgttgcgat gattcggaat gcggctattc atgctggcct tgctgttatg gataagcttt 240

gttatcgcgg cctcatccag tgtcaacgaa taagtaaaac gattgcagt 289

<210> 330
<211> 70
<212> PRT
<213> Conus ammiralis

<400> 330
Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
20 25 30

Ala Glu Arg Leu Gln Asp Arg Ile Pro Thr Glu Asp His Pro Leu Phe
35 40 45

Asp Pro Asn Lys Arg Cys Cys Asp Asp Ser Glu Cys Gly Tyr Ser Cys
50 55 60

Trp Pro Cys Cys Tyr Gly
65 70

<210> 331
<211> 16
<212> PRT
<213> Conus ammiralis

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue6 is Glu or gamma-carboxy Glu; Xaa at residue 13 i
s Pro or Hyp; Xaa at residue 12 is Trp or bromo-Trp; Xaa at resid
ue 9 and 16 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulph
o-Tyr or O-phospho-Ty

<400> 331
Cys Cys Asp Asp Ser Xaa Cys Gly Xaa Ser Cys Xaa Xaa Cys Cys Xaa
1 5 10 15

<210> 332
<211> 272
<212> DNA
<213> Conus spurius

<400> 332
caagaaggat cgatagcagt tcatgatgtc taaactggga gtcttgctga ccatctgtct 60

gcttctgttt ccacgtactt ctcttccgct ggatggagat caacctgcag tccgatctgc 120

aaagcgtatg cattcatcta tacagcgtcg tttctttgat cccgtcaaac ggtgttgccc 180

tagatgcagc gagtgcaacc cttgttgtgg atgaccagct ttgtcatcgc ggcctcatta 240

agtgtctaat gaataagtaa aatgattgca gt 272

<210> 333
<211> 63
<212> PRT
<213> Conus spurius

<400> 333
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Arg Thr Ser Leu Pro Leu Asp Gly Asp Gln Pro Ala Val Arg Ser
20 25 30

Ala Lys Arg Met His Ser Ser Ile Gln Arg Arg Phe Phe Asp Pro Val
35 40 45

Lys Arg Cys Cys Pro Arg Cys Ser Glu Cys Asn Pro Cys Cys Gly
50 55 60

<210> 334
<211> 12
<212> PRT
<213> Conus spurius

<220>
<221> PEPTIDE
<222> (1)..(12)
<223> Xaa at residue 7 is Glu or gamma-carboxy Glu; Xaa at residue 3 an
d 10 is Pro or Hy

<400> 334
Cys Cys Xaa Arg Cys Ser Xaa Cys Asn Xaa Cys Cys
1 5 10

<210> 335
<211> 293
<212> DNA
<213> Conus omaria

<400> 335
caagagggat cgatagcagt tcatgatgtc taaactggga gtctcgttga ccatctgtct 60

acttctattt tcccttactg ctgttccgct tgatggagat caacatgcag accaacctgc 120

agagcgtctg cagggcgaca ttttatctga aaagcatccc ttatttaatc ccgtcaaacg 180

gtgttgcgat gaggaagaat gcagcagtgc atgctggcct tgttgttggg ggtgatcagc 240

tttgttatcg cggcctcatc aagtgtctaa tgaataagta aaatgattgc agt 293

<210> 336
<211> 70
<212> PRT
<213> Conus omaria

<400> 336
Met Met Ser Lys Leu Gly Val Ser Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
20 25 30

Ala Glu Arg Leu Gln Gly Asp Ile Leu Ser Glu Lys His Pro Leu Phe
35 40 45

Asn Pro Val Lys Arg Cys Cys Asp Glu Glu Glu Cys Ser Ser Ala Cys
50 55 60

Trp Pro Cys Cys Trp Gly
65 70

<210> 337
<211> 16
<212> PRT
<213> Conus omaria

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 4, 5 and 6 is Glu or gamma-carboxy Glu; Xaa at res
idue 13 is Pro or Hyp; Xaa at residue 12 and 16 is Trp or bromo-T
r

<400> 337
Cys Cys Asp Xaa Xaa Xaa Cys Ser Ser Ala Cys Xaa Xaa Cys Cys Xaa
1 5 10 15

<210> 338
<211> 293
<212> DNA
<213> Conus omaria

<400> 338
caagaaggat cgatagcagt tcatgatgtc taaactggga gtcttgttga tcatctgtct 60

acttctgtgt ccccttactg ctgttctgga ggatggagat caacctgcag accgacctgc 120

agagcgtatg caggacgaca tttcaactga gcatcatccc ttttatgatc ccgtcaaacg 180

gtgttgcaag tacgggtgga catgcttgct aggatgcact ccttgtgatt gttgaccagt 240

tttgttatcg cggcctcgtc aagtgtctaa tgaataagta aaacgattgc agt 293

<210> 339
<211> 70
<212> PRT
<213> Conus omaria

<400> 339
Met Met Ser Lys Leu Gly Val Leu Leu Ile Ile Cys Leu Leu Leu Cys
1 5 10 15

Pro Leu Thr Ala Val Leu Glu Asp Gly Asp Gln Pro Ala Asp Arg Pro
20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Thr Glu His His Pro Phe Tyr
35 40 45

Asp Pro Val Lys Arg Cys Cys Lys Tyr Gly Trp Thr Cys Leu Leu Gly
50 55 60

Cys Thr Pro Cys Asp Cys
65 70

<210> 340
<211> 17
<212> PRT
<213> Conus omaria

<220>
<221> PEPTIDE
<222> (1)..(17)
<223> Xaa at residue is 14 Pro or Hyp; Xaa at residue 6 is Trp or bromo -Trp; Xaa at residue 4 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-T yr, O-sulpho-Tyr or O-phospho-Ty

<400> 340
Cys Cys Lys Xaa Gly Xaa Thr Cys Leu Leu Gly Cys Thr Xaa Cys Asp
1 5 10 15

Cys

<210> 341
<211> 290
<212> DNA
<213> Conus omaria

<400> 341
caagagggat cgatagcagt tcatgatgtc tatactggga gtcttgttga tcatctgtct 60

acttctgtgt ccccttactg ctgttctgga ggatggagat caacctgcag accgacctgc 120

agagcgtatg caggacggca tttcatctga acatcatccc tttttggatc ccgtcaaacg 180

gtgttgccat ctattggcat gccgctttgg atgctcgcct tgttgttggt gaccagcttt 240

gttatcgcgg cctcatcaag tgtctaatga ataagtaaaa cgattgcagt 290

<210> 342
<211> 69
<212> PRT
<213> Conus omaria

<400> 342
Met Met Ser Ile Leu Gly Val Leu Leu Ile Ile Cys Leu Leu Leu Cys
1 5 10 15
Pro Leu Thr Ala Val Leu Glu Asp Gly Asp Gln Pro Ala Asp Arg Pro
20 25 30

Ala Glu Arg Met Gln Asp Gly Ile Ser Ser Glu His His Pro Phe Leu
35 40 45

Asp Pro Val Lys Arg Cys Cys His Leu Leu Ala Cys Arg Phe Gly Cys
50 55 60

Ser Pro Cys Cys Trp
65

<210> 343
<211> 16
<212> PRT
<213> Conus omaria

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 13 is Pro or Hyp; Xaa at residue 16 is Trp or brom o-Tr

<400> 343
Cys Cys His Leu Leu Ala Cys Arg Phe Gly Cys Ser Xaa Cys Cys Xaa
1 5 10 15

<210> 344
<211> 293
<212> DNA
<213> Conus omaria

<400> 344
caagaaggat cgatagcagt tcatgatgtc taaactggga gtcttgttga tcatctgtct 60

acttctttgt ccccttactg ctgttccgca ggatggagat caacctgcag accgacctgc 120

agagcgtatg cagggcggca tttcatctga acatcatccc ttttttgatc ccgtcaaacg 180

gtgttgcagg tacgggtgga catgctggct aggatgcact ccctgtggtt gttgaccagc 240

tttgttatcg cggcctcatc aagtgtctaa tgaataagta aaacgattgc agt 293

<210> 345
<211> 70
<212> PRT
<213> Conus omaria

<400> 345
Met Met Ser Lys Leu Gly Val Leu Leu Ile Ile Cys Leu Leu Leu Cys
1 5 10 15

Pro Leu Thr Ala Val Pro Gln Asp Gly Asp Gln Pro Ala Asp Arg Pro
20 25 30

Ala Glu Arg Met Gln Gly Gly Ile Ser Ser Glu His His Pro Phe Phe
35 40 45

Asp Pro Val Lys Arg Cys Cys Arg Tyr Gly Trp Thr Cys Trp Leu Gly
50 55 60

Cys Thr Pro Cys Gly Cys
65 70

<210> 346
<211> 17
<212> PRT
<213> Conus omaria

<220>
<221> PEPTIDE
<222> (1)..(17)
<223> Xaa at residue 14 is Pro or Hyp; Xaa at residue 6 and 9 is Trp or bromo-Trp; Xaa at residue 4 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 346
Cys Cys Arg Xaa Gly Xaa Thr Cys Xaa Leu Gly Cys Thr Xaa Cys Gly
1 5 10 15

Cys

<210> 347
<211> 293
<212> DNA
<213> Conus episcopatus

<400> 347
caagaaggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct 60

acttctgttt tcccttattg ctgttccgct tgatggagat caacatgcag accaacctgc 120

agagcgtctg cagggcgaca ttttatctga aaagcatccc ttatttatgc ctgtcaaacg 180

gtgttgcgat gaggacgaat gcaacagttc atgctggcct tgttgttggg ggtgatcagc 240

tttgttatcg cggcctgatc aagtgtataa tgaataagta aaacgattgc agt 293

<210> 348
<211> 70
<212> PRT
<213> Conus episcopatus

<400> 348
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Ser Leu Ile Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
20 25 30

Ala Glu Arg Leu Gln Gly Asp Ile Leu Ser Glu Lys His Pro Leu Phe
35 40 45

Met Pro Val Lys Arg Cys Cys Asp Glu Asp Glu Cys Asn Ser Ser Cys
50 55 60

Trp Pro Cys Cys Trp Gly
65 70

<210> 349
<211> 16
<212> PRT
<213> Conus episcopatus

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 4 and 6 is Glu or gamma-carboxy Glu; Xaa at residu
e 13 is Pro or Hyp; Xaa at residue 12 and 16 is Trp or bromo-Trp

<400> 349
Cys Cys Asp Xaa Asp Xaa Cys Asn Ser Ser Cys Xaa Xaa Cys Cys Xaa
1 5 10 15

<210> 350
<211> 293
<212> DNA
<213> Conus episcopatus

<400> 350
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct 60

acttctgttt tcccttattg ctgttccgct tgatggagat caacatgcag accaacctgc 120

agagcgtctg cagggcgaca ttttatctga aaagcatccc ttatttatgc ctgtcaaacg 180

gtgttgcgat gaggacgaat gcagcagttc atgctggcct tgttgttggg gatgagcagc 240

tttgttatcg cggcctcatc aagtgtctaa tgaataagta aaacgattgc agt 293

<210> 351
<211> 70

<212> PRT
<213> Conus episcopatus

<400> 351
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Ser Leu Ile Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
20 25 30

Ala Glu Arg Leu Gln Gly Asp Ile Leu Ser Glu Lys His Pro Leu Phe
35 40 45

Met Pro Val Lys Arg Cys Cys Asp Glu Asp Glu Cys Ser Ser Ser Cys
50 55 60

Trp Pro Cys Cys Trp Gly
65 70

<210> 352
<211> 16
<212> PRT
<213> Conus episcopatus

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue4 and 6 is Glu or gamma-carboxy Glu; Xaa at residu
e 13 is Pro or Hyp; Xaa at residue 12 and 16 is Trp or bromo-Trp

<400> 352
Cys Cys Asp Xaa Asp Xaa Cys Ser Ser Ser Cys Xaa Xaa Cys Cys Xaa
1 5 10 15

<210> 353
<211> 290
<212> DNA
<213> Conus episcopatus

<400> 353
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct 60

acttctgttt tcccttactg ctgttccgct tgatggagat caacatgcag accaacctgc 120

agagcgtctg cagggcgaca ttttatctga aaagcatccc ttatttaatc ccgtcaaacg 180

gtgttgcccg gcggcggcat gtgccatggg atgcaagcct tgttgtggat gagcagcttt 240

gttatcgtgg cctcatcaag tgtctaatga ataagtaaaa cgattgcagt 290

<210> 354
<211> 69
<212> PRT
<213> Conus episcopatus

<400> 354
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
20 25 30

Ala Glu Arg Leu Gln Gly Asp Ile Leu Ser Glu Lys His Pro Leu Phe
35 40 45

```
Asn Pro Val Lys Arg Cys Cys Pro Ala Ala Ala Cys Ala Met Gly Cys
    50                  55                  60

Lys Pro Cys Cys Gly
65

<210>  355
<211>  15
<212>  PRT
<213>  Conus episcopatus

<220>
<221>  PEPTIDE
<222>  (1)..(15)
<223>  Xaa at residue 3 and 13 is Pro or Hyp

<400>  355
Cys Cys Xaa Ala Ala Ala Cys Ala Met Gly Cys Lys Xaa Cys Cys
1               5                   10                  15

<210>  356
<211>  295
<212>  DNA
<213>  Conus aulicus

<400>  356
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct      60
gcttctgttt tccgttactg ctcttccgcc ggatggagat caacctgcag accgagctgc     120

agagcgtagg caggtcgagc agcatcccgt gtttgatcat gaaagagggt gttgctcgcc     180

accatgccac agtatttgcg ctgctttctg ttgcgggtga tgataacgtg ttgatgaccc     240

actttgtcat cacggctgcg tcaagtgtct aatgaataag taaaatgatt gcagt          295

<210>  357
<211>  65
<212>  PRT
<213>  Conus aulicus

<400>  357
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1               5                   10                  15

Ser Val Thr Ala Leu Pro Pro Asp Gly Asp Gln Pro Ala Asp Arg Ala
            20                  25                  30

Ala Glu Arg Arg Gln Val Glu Gln His Pro Val Phe Asp His Glu Arg
        35                  40                  45

Gly Cys Cys Ser Pro Pro Cys His Ser Ile Cys Ala Ala Phe Cys Cys
    50                  55                  60

Gly
65

<210>  358
<211>  16
<212>  PRT
<213>  Conus aulicus

<220>
<221>  PEPTIDE
<222>  (1)..(16)
<223>  Xaa at residue 5 and 6 is Pro or Hyp
```

<400> 358
Gly Cys Cys Ser Xaa Xaa Cys His Ser Ile Cys Ala Ala Phe Cys Cys
1 5 10 15

<210> 359
<211> 290
<212> DNA
<213> Conus aulicus

<400> 359
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct 60

acttctgttt tcccttactg ctgttccgct tgatggagat caacatgcag accaacctgc 120

agagcgtctg cagggcgaca ttttatctga aaagcatccc ttatttaatc ccgtcaaacg 180

gtgttgccga ccggtggcat gtgccatggg atgcaagcct tgttgtggat gagcagcttt 240

gttatcgtgg cctcatcaag tgtctaatga ataagtaaaa tgattgcagt 290

<210> 360
<211> 69
<212> PRT
<213> Conus aulicus

<400> 360
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
20 25 30

Ala Glu Arg Leu Gln Gly Asp Ile Leu Ser Glu Lys His Pro Leu Phe
35 40 45

Asn Pro Val Lys Arg Cys Cys Arg Pro Val Ala Cys Ala Met Gly Cys
50 55 60

Lys Pro Cys Cys Gly
65

<210> 361
<211> 15
<212> PRT
<213> Conus aulicus

<220>
<221> PEPTIDE
<222> (1)..(15)
<223> Xaa at residue 4 and 13 is Pro or Hyp

<400> 361
Cys Cys Arg Xaa Val Ala Cys Ala Met Gly Cys Lys Xaa Cys Cys
1 5 10 15

<210> 362
<211> 290
<212> DNA
<213> Conus aulicus

<400> 362
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga tcatctgtct 60

acttctgtct ccccttactg ctgttccgct ggatggagat caacctgcag accgacctgc 120

agagcgtatg caggacgaca tttcatctga acatcaaccc atgtttgatg ccatcagaca 180

gtgttgcccg gcggtggcat gcgccatggg atgcgagcct tgttgtggat gaccagcttt 240

gttatcgcgg cctcatcaag tgtctaatga ataagtaaaa tgattgcagt 290

<210> 363
<211> 69
<212> PRT
<213> Conus aulicus

<400> 363
Met Met Ser Lys Leu Gly Val Leu Leu Ile Ile Cys Leu Leu Leu Ser
1 5 10 15

Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro
20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu His Gln Pro Met Phe
35 40 45

Asp Ala Ile Arg Gln Cys Cys Pro Ala Val Ala Cys Ala Met Gly Cys
50 55 60

Glu Pro Cys Cys Gly
65

<210> 364
<211> 16
<212> PRT
<213> Conus aulicus

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 13 is Glu or gamma-carboxy Glu; Xaa at residue 4 and 14 is Pro or Hy

<400> 364
Xaa Cys Cys Xaa Ala Val Ala Cys Ala Met Gly Cys Xaa Xaa Cys Cys
1 5 10 15

<210> 365
<211> 293
<212> DNA
<213> Conus aureus

<400> 365
caagaaggat cgatagcagt tcatgatgtc taaactggga gccttgttga ccatctgtct 60

acttctgttt tcccttactg ctgttccgct ggatggagat caacatgcag accaacatgc 120

agagcgtctg catgaccgcc ttccaactga aaatcatccc ttatatgatc ccgtcaaacg 180

gtgttgcgat gattcggaat gcgactattc ttgctggcct tgctgtattt ttggataacc 240

tttgttatcg cggcctcatc aagtgtcaaa tgaataagta aaacgattgc agt 293

<210> 366
<211> 71
<212> PRT
<213> Conus aureus

<400> 366

Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln His
20 25 30

Ala Glu Arg Leu His Asp Arg Leu Pro Thr Glu Asn His Pro Leu Tyr
35 40 45

Asp Pro Val Lys Arg Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys
50 55 60

Trp Pro Cys Cys Ile Phe Gly
65 70

<210> 367
<211> 17
<212> PRT
<213> Conus aureus

<220>
<221> PEPTIDE
<222> (1)..(17)
<223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 i
s Pro or Hyp; Xaa at residue 12 is Trp or bromo-Trp; Xaa at resid
ue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr o
r O-phospho-Ty

<400> 367
Cys Cys Asp Asp Ser Xaa Cys Asp Xaa Ser Cys Xaa Xaa Cys Cys Ile
1 5 10 15

Phe

<210> 368
<211> 290
<212> DNA
<213> Conus aureus

<400> 368
caagagggat cgatagcagt tcatgatgtc taaactggga gccttgttga ccatctgtct 60

acttctgttt tccctaactg ctgttccgct ggatggagat caacatgcag accaacctgc 120

agagcgtctg caggaccgca ttccaactga aaatcatccc ttatttgatc cgaacaaacg 180

gtgttgcaat gattgggaat gcgacgattc atgctggcct tgctgttatg gataaccttt 240

gttatcgcgg cctcatcaag tgtcaaatga ataagtaaaa cgattgcagt 290

<210> 369
<211> 70
<212> PRT
<213> Conus aureus

<400> 369
Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
20 25 30

Ala Glu Arg Leu Gln Asp Arg Ile Pro Thr Glu Asn His Pro Leu Phe
35 40 45

Asp Pro Asn Lys Arg Cys Cys Asn Asp Trp Glu Cys Asp Asp Ser Cys
    50   55   60

Trp Pro Cys Cys Tyr Gly
65   70

<210> 370
<211> 16
<212> PRT
<213> Conus aureus

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 is Pro or Hyp; Xaa at residue 5 and 12 is Trp or bromo-Trp; Xaa at residue 16 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 370
Cys Cys Asn Asp Xaa Xaa Cys Asp Asp Ser Cys Xaa Xaa Cys Cys Xaa
1   5   10   15

<210> 371
<211> 310
<212> DNA
<213> Conus consors

<400> 371
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgttt 60

gcttctgttt ccccttactg ctcttccaat ggatggagat caatctgtag accgacctgc 120

agagcgtatg caggacgaca tttcatctga gctgcatccc ttgttcaatc agaaaagaat 180

gtgttgcggc gaaggtgcgc catgccccag ctatttcaga aacagtcaga tttgtcattg 240

ttgttaaatg acaacgtgtc gatgaccaac ttcgttatca cgactaatga ataagtaaaa 300

tgattgcagt 310

<210> 372
<211> 74
<212> PRT
<213> Conus consors

<400> 372
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1   5   10   15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Ser Val Asp Arg Pro
            20   25   30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Leu His Pro Leu Phe
        35   40   45

Asn Gln Lys Arg Met Cys Cys Gly Glu Gly Ala Pro Cys Pro Ser Tyr
    50   55   60

Phe Arg Asn Ser Gln Ile Cys His Cys Cys
65   70

<210> 373
<211> 22
<212> PRT

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<213>  Conus consors

<220>
<221>  PEPTIDE
<222>  (1)..(22)
<223>  Xaa at residue 5 is Glu or gamma-carboxy Glu; Xaa at residue 8 an
       d 10 is Pro or Hyp; Xaa at residue 12 is Tyr, 125I-Tyr, mono-iodo
       -Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400>  373
Met Cys Cys Gly Xaa Gly Ala Xaa Cys Xaa Ser Xaa Phe Arg Asn Ser
1               5                   10                  15

Gln Ile Cys His Cys Cys
            20

<210>  374
<211>  315
<212>  DNA
<213>  Conus consors

<400>  374
taagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct      60

gcttctgttt ccccttattg ctcttccaat ggatggagat caacctgcag accgacctgc     120

agagcgtatg caggacgaca tttcatctca gcagcatccc ttgtttgata agagaggccg     180

ctgttgcgat gtgccgaacg catgctccgg cagatggtgc agagatcacg cacaatgttg     240

cggatgacga taacgtgttg atgaccaact ttgtgatcac ggctacatca agtgaataag     300

taaaacgatt gcagt                                                      315

<210>  375
<211>  74
<212>  PRT
<213>  Conus consors

<400>  375
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1               5                   10                  15

Pro Leu Ile Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Pro
            20                  25                  30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Gln Gln His Pro Leu Phe
        35                  40                  45

Asp Lys Arg Gly Arg Cys Cys Asp Val Pro Asn Ala Cys Ser Gly Arg
    50                  55                  60

Trp Cys Arg Asp His Ala Gln Cys Cys Gly
65                  70

<210>  376
<211>  22
<212>  PRT
<213>  Conus consors

<220>
<221>  PEPTIDE
<222>  (1)..(22)
<223>  Xaa at residue 7 is Pro or Hyp; Xaa at residue 14 is Trp or bromo
       -Tr
```

<400> 376
Gly Arg Cys Cys Asp Val Xaa Asn Ala Cys Ser Gly Arg Xaa Cys Arg
1 5 10 15

Asp His Ala Gln Cys Cys
20

<210> 377
<211> 322
<212> DNA
<213> Conus consors

<400> 377
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ctgtctgttt 60

gcttctgttt ccccttactg ctcttccgat ggatggagat caacctgcag accaacctgc 120

agagcgtatg caggacgaca tttcatctga gcagcatccc ttgtttgata agagacaaag 180

gtgttgcact gggaagaagg ggtcatgctc cggtaaagca tgcaaaagtc tcaaatgttg 240

ctctggacga taacgtgttg atgaccaact ttgttatcac ggctacgtca agtgtctagt 300

gaataagtaa aacgattgca gt 322

<210> 378
<211> 76
<212> PRT
<213> Conus consors

<400> 378
Met Met Ser Lys Leu Gly Val Leu Leu Thr Val Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro
20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln His Pro Leu Phe
35 40 45

Asp Lys Arg Gln Arg Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly
50 55 60

Lys Ala Cys Lys Ser Leu Lys Cys Cys Ser Gly Arg
65 70 75

<210> 379
<211> 23
<212> PRT
<213> Conus consors

<220>
<221> PEPTIDE
<222> (1)..(23)
<223> Xaa at residue 1 is Gln or pyro-Glu

<400> 379
Xaa Arg Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys Ala Cys
1 5 10 15

Lys Ser Leu Lys Cys Cys Ser
20

<210> 380

<211> 284
<212> DNA
<213> Conus emaciatus

<400> 380
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgctga ccatctgtct 60

gcttctgttt ccccttactg ttcttccgat ggatggagat caacctgcag acctacctgc 120

attgcgtgcg cagttctttg cacctgaaca tagtccccgg tttgaccccg tcaaacggtg 180

ctgctcgcgg gattgcagtg tttgcatccc ttgttgcccg tatggatcac cttgattatt 240

gcggccacgt caagtgtcta atgaataagt aaaatgattg cagt 284

<210> 381
<211> 70
<212> PRT
<213> Conus emaciatus

<400> 381
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Val Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Leu Pro
20 25 30

Ala Leu Arg Ala Gln Phe Phe Ala Pro Glu His Ser Pro Arg Phe Asp
35 40 45

Pro Val Lys Arg Cys Cys Ser Arg Asp Cys Ser Val Cys Ile Pro Cys
50 55 60

Cys Pro Tyr Gly Ser Pro
65 70

<210> 382
<211> 18
<212> PRT
<213> Conus emaciatus

<220>
<221> PEPTIDE
<222> (1)..(18)
<223> Xaa at residue 11, 14 and 18 is Pro or Hyp; Xaa at residue 15 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phos pho-Ty

<400> 382
Cys Cys Ser Arg Asp Cys Ser Val Cys Ile Xaa Cys Cys Xaa Xaa Gly
1 5 10 15

Ser Xaa

<210> 383
<211> 13
<212> PRT
<213> Conus aurisiacus

<400> 383
Cys Cys Lys Val Gln Cys Glu Ser Cys Thr Pro Cys Cys
1 5 10

<210> 384
<211> 15

<212> PRT
<213> Conus atlanticus

<400> 384
Cys Cys Glu Leu Pro Cys Gly Pro Gly Phe Cys Val Pro Cys Cys
1 5 10 15

<210> 385
<211> 14
<212> PRT
<213> Conus arentus

<400> 385
Cys Cys Glu Arg Pro Cys Asn Ile Gly Cys Val Pro Cys Cys
1 5 10

<210> 386
<211> 16
<212> PRT
<213> Conus bandus

<400> 386
Cys Cys Asn Trp Pro Cys Ser Met Gly Cys Ile Pro Cys Cys Tyr Tyr
1 5 10 15

<210> 387
<211> 15
<212> PRT
<213> Conus betulinus

<400> 387
Cys Cys Glu Leu Pro Cys His Gly Cys Val Pro Cys Cys Trp Pro
1 5 10 15

<210> 388
<211> 16
<212> PRT
<213> Conus betulinus

<400> 388
Cys Cys Gly Leu Pro Cys Asn Gly Cys Val Pro Cys Cys Trp Pro Ser
1 5 10 15

<210> 389
<211> 18
<212> PRT
<213> Conus betulinus

<400> 389
Cys Cys Ser Arg Asn Cys Ala Val Cys Ile Pro Cys Cys Pro Asn Trp
1 5 10 15

Pro Ala

<210> 390
<211> 14
<212> PRT
<213> Conus betulinus

<400> 390
Cys Cys Lys Gln Ser Cys Thr Thr Cys Met Pro Cys Cys Trp
1 5 10

<210> 391
<211> 14

<212> PRT
<213> Conus betulinus

<220>
<221> PEPTIDE
<222> (1)..(14)
<223> Xaa is Glu or gamma-carboxy Glu

<400> 391
Ala Cys Cys Xaa Gln Ser Cys Thr Thr Cys Met Pro Cys Cys
1 5 10

<210> 392
<211> 14
<212> PRT
<213> Conus betulinus

<400> 392
Cys Cys Glu Gln Ser Cys Thr Thr Cys Met Pro Cys Cys Trp
1 5 10

<210> 393
<211> 18
<212> PRT
<213> Conus caracteristicus

<400> 393
Arg Cys Cys Arg Tyr Pro Cys Pro Asp Ser Cys His Gly Ser Cys Cys
1 5 10 15

Tyr Lys

<210> 394
<211> 15
<212> PRT
<213> Conus caracteristicus

<400> 394
Cys Cys Pro Pro Val Ala Cys Asn Met Gly Cys Lys Pro Cys Cys
1 5 10 15

<210> 395
<211> 17
<212> PRT
<213> Conus caracteristicus

<400> 395
Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys Trp Pro Cys Cys Met
1 5 10 15

Phe

<210> 396
<211> 14
<212> PRT
<213> Conus caracteristicus

<400> 396
Cys Cys Arg Arg Cys Tyr Met Gly Cys Ile Pro Cys Cys Phe
1 5 10

<210> 397
<211> 16
<212> PRT
<213> Conus textile

<400> 397
Cys Cys Pro Pro Val Ala Cys Asn Met Gly Cys Lys Pro Cys Cys Gly
1 5 10 15

<210> 398
<211> 19
<212> PRT
<213> Conus marmoreus

<220>
<221> PEPTIDE
<222> (1)..(19)
<223> Xaa is Hyp

<400> 398
Ser Lys Gln Cys Cys His Leu Ala Ala Cys Arg Phe Gly Cys Thr Xaa
1 5 10 15

Cys Cys Asn

<210> 399
<211> 15
<212> PRT
<213> Conus capitaneus

<400> 399
Ser Cys Cys Arg Asp Cys Gly Glu Asp Cys Val Gly Cys Cys Arg
1 5 10 15

<210> 400
<211> 16
<212> PRT
<213> Conus coronatus

<400> 400
Cys Cys Asp Trp Pro Cys Ile Pro Gly Cys Thr Pro Cys Cys Leu Pro
1 5 10 15

<210> 401
<211> 18
<212> PRT
<213> Conus dalli

<400> 401
Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys Trp Pro Cys Cys Ile
1 5 10 15

Leu Ser

<210> 402
<211> 17
<212> PRT
<213> Conus dalli

<400> 402
Glx Gln Cys Cys Pro Pro Val Ala Cys Asn Met Gly Cys Glu Pro Cys
1 5 10 15

Cys

<210> 403
<211> 16
<212> PRT
<213> Conus dalli

<400> 403
Cys Cys Asn Ala Gly Phe Cys Arg Phe Gly Cys Thr Pro Cys Cys Trp
1 5 10 15

<210> 404
<211> 14
<212> PRT
<213> Conus distans

<400> 404
Glx Cys Cys Val His Pro Cys Pro Cys Thr Pro Cys Cys Arg
1 5 10

<210> 405
<211> 14
<212> PRT
<213> Conus figulinus

<400> 405
Cys Cys Pro Trp Pro Cys Asn Ile Gly Cys Val Pro Cys Cys
1 5 10

<210> 406
<211> 14
<212> PRT
<213> Conus figulinus

<400> 406
Cys Cys Ser Lys Asn Cys Ala Val Cys Ile Pro Cys Cys Pro
1 5 10

<210> 407
<211> 15
<212> PRT
<213> Conus figulinus

<400> 407
Cys Cys Arg Trp Pro Cys Pro Ala Arg Cys Gly Ser Cys Cys Leu
1 5 10 15

<210> 408
<211> 16
<212> PRT
<213> Conus figulinus

<400> 408
Cys Cys Glu Leu Ser Arg Cys Leu Gly Cys Val Pro Cys Cys Thr Ser
1 5 10 15

<210> 409
<211> 16
<212> PRT
<213> Conus figulinus

<400> 409
Cys Cys Glu Leu Ser Lys Cys His Gly Cys Val Pro Cys Cys Ile Pro
1 5 10 15

<210> 410
<211> 16
<212> PRT
<213> Conus generalis

<400> 410

Glx Cys Cys Thr Phe Cys Asn Phe Gly Cys Gln Pro Cys Cys Val Pro
1 5 10 15

<210> 411
<211> 16
<212> PRT
<213> Conus generalis

<400> 411
Glx Cys Cys Thr Phe Cys Asn Phe Gly Cys Gln Pro Cys Cys Leu Thr
1 5 10 15

<210> 412
<211> 16
<212> PRT
<213> Conus generalis

<400> 412

Glx Cys Cys Thr Phe Cys Asn Phe Gly Cys Gln Pro Cys Cys Val Pro
1 5 10 15
<210> 413
<211> 17
<212> PRT
<213> Conus gloriamaris

<400> 413
Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys Trp Pro Cys Cys Met
1 5 10 15

Phe

<210> 414
<211> 17
<212> PRT
<213> Conus gloriamaris

<400> 414
Gly Cys Cys His Leu Leu Ala Cys Arg Phe Gly Cys Ser Pro Cys Cys
1 5 10 15
Trp

<210> 415
<211> 16
<212> PRT
<213> Conus gloriamaris

<400> 415
Cys Cys Ser Trp Asp Val Cys Asp His Pro Ser Cys Thr Cys Cys Gly
1 5 10 15

<210> 416
<211> 13
<212> PRT
<213> Conus laterculatus

<400> 416
Cys Cys Asp Trp Pro Cys Ser Gly Cys Ile Pro Cys Cys
1 5 10

<210> 417
<211> 19
<212> PRT
<213> Conus leopardus

<400> 417
Glx Ile Asn Cys Cys Pro Trp Pro Cys Pro Ser Thr Cys Arg His Gln
1 5 10 15

Cys Cys His

<210> 418
<211> 19
<212> PRT
<213> Conus lividus

<400> 418
Glx Ile Asn Cys Cys Pro Trp Pro Cys Pro Asp Ser Cys His Tyr Gln
1 5 10 15

Cys Cys His

<210> 419
<211> 14
<212> PRT
<213> Conus marmoreus

<400> 419
Cys Cys Arg Leu Ser Cys Gly Leu Gly Cys His Pro Cys Cys
1 5 10

<210> 420
<211> 17
<212> PRT
<213> Conus marmoreus

<400> 420
Glu Cys Cys Gly Ser Phe Ala Cys Arg Phe Gly Cys Val Pro Cys Cys
1 5 10 15

Val

<210> 421
<211> 19
<212> PRT
<213> Conus marmoreus

<400> 421
Ser Lys Gln Cys Cys His Leu Pro Ala Cys Arg Phe Gly Cys Thr Pro
1 5 10 15

Cys Cys Trp

<210> 422
<211> 17
<212> PRT
<213> Conus marmoreus

<400> 422
Met Gly Cys Cys Pro Phe Pro Cys Lys Thr Ser Cys Thr Thr Leu Cys
1 5 10 15

Cys

<210> 423
<211> 14
<212> PRT
<213> Conus musicus

<400> 423

Ala Cys Cys Glu Gln Ser Cys Thr Thr Cys Phe Pro Cys Cys
1 5 10

<210> 424
<211> 15
<212> PRT
<213> Conus nobilis

<400> 424
Cys Cys Glu Leu Pro Cys Gly Pro Gly Phe Cys Val Pro Cys Cys
1 5 10 15

<210> 425
<211> 14
<212> PRT
<213> Conus pulicarius

<400> 425
Cys Cys Asn Ser Cys Tyr Met Gly Cys Ile Pro Cys Cys Phe
1 5 10

<210> 426
<211> 17
<212> PRT
<213> Conus quercinus

<400> 426
Glx Arg Cys Cys Gln Trp Pro Cys Pro Gly Ser Cys Arg Cys Cys Arg
1 5 10 15

Thr

<210> 427
<211> 18
<212> PRT
<213> Conus quercinus

<400> 427
Glx Arg Cys Cys Arg Trp Pro Cys Pro Gly Ser Cys Arg Cys Cys Arg
1 5 10 15

Tyr Arg

<210> 428
<211> 18
<212> PRT
<213> Conus quercinus

<400> 428
Arg Cys Cys Arg Tyr Pro Cys Pro Asp Ser Cys His Gly Ser Cys Cys
1 5 10 15

Tyr Lys

<210> 429
<211> 15
<212> PRT
<213> Conus quercinus

<220>
<221> PEPTIDE
<222> (1)..(15)
<223> Xaa is Hyp

<400> 429

Cys Cys Ser Gln Asp Cys Leu Val Cys Ile Xaa Cys Cys Pro Asn
1 5 10 15

<210> 430
<211> 15
<212> PRT
<213> Conus quercinus

<220>
<221> PEPTIDE
<222> (1)..(15)
<223> Xaa is Hyp

<400> 430
Cys Cys Ser Arg His Cys Trp Val Cys Ile Xaa Cys Cys Pro Asn
1 5 10 15

<210> 431
<211> 16
<212> PRT
<213> Conus rattus

<400> 431
Glx Thr Cys Cys Ser Asn Cys Gly Glu Asp Cys Asp Gly Cys Cys Gln
1 5 10 15

<210> 432
<211> 20
<212> PRT
<213> Conus striatus

<400> 432
Glx Asn Cys Cys Asn Gly Gly Cys Ser Ser Lys Trp Cys Arg Asp His
1 5 10 15

Ala Arg Cys Cys
20

<210> 433
<211> 12
<212> PRT
<213> Conus textile

<220>
<221> PEPTIDE
<222> (1)..(12)
<223> Xaa is Hyp

<400> 433
Cys Cys Arg Thr Cys Phe Gly Cys Thr Xaa Cys Cys
1 5 10

<210> 434
<211> 14
<212> PRT
<213> Conus tessulatus

<400> 434
Cys Cys His Lys Cys Tyr Met Gly Cys Ile Pro Cys Cys Ile
1 5 10

<210> 435
<211> 18
<212> PRT
<213> Conus tessulatus

<400> 435
Lys Cys Cys Arg Pro Pro Cys Ala Met Ser Cys Gly Met Ala Arg Cys
1 5 10 15

Cys Tyr

<210> 436
<211> 23
<212> PRT
<213> Conus betulinus

<400> 436
Arg Cys Cys Arg Trp Pro Cys Pro Ser Ile Cys Gly Met Ala Arg Cys
1 5 10 15

Cys Phe Val Met Ile Thr Cys
20

<210> 437
<211> 23
<212> PRT
<213> Conus betulinus

<400> 437
Arg Cys Cys Arg Trp Pro Cys Pro Ser Arg Cys Gly Met Ala Arg Cys
1 5 10 15

Cys Phe Val Met Ile Thr Cys
20

<210> 438
<211> 15
<212> PRT
<213> Conus textile

<400> 438
Phe Cys Cys Asp Ser Asn Trp Cys His Asp Cys Glu Cys Cys Tyr
1 5 10 15

<210> 439
<211> 16
<212> PRT
<213> Conus marmoreus

<400> 439
Cys Cys His Trp Asn Trp Cys Asp His Leu Cys Ser Cys Cys Gly Ser
1 5 10 15

<210> 440
<211> 16
<212> PRT
<213> Conus marmoreus

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa is Hyp

<400> 440
Asp Cys Cys Xaa Leu Pro Ala Cys Pro Phe Gly Cys Asn Xaa Cys Cys
1 5 10 15

<210> 441
<211> 16

<212> PRT
<213> Conus marmoreus

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa is Hyp

<400> 441
Cys Cys Ala Pro Ser Ala Cys Arg Leu Gly Cys Arg Xaa Cys Cys Arg
1 5 10 15

<210> 442
<211> 16
<212> PRT
<213> Conus marmoreus

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa is Hyp

<400> 442
Cys Cys Ala Xaa Ser Ala Cys Arg Leu Gly Cys Arg Xaa Cys Cys Arg
1 5 10 15

<210> 443
<211> 16
<212> PRT
<213> Conus marmoreus

<400> 443
Cys Cys Ala Pro Ser Ala Cys Arg Leu Gly Cys Arg Pro Cys Cys Arg
1 5 10 15

<210> 444
<211> 17
<212> PRT
<213> Conus marmoreus

<220>
<221> PEPTIDE
<222> (1)..(17)
<223> Xaa is Hyp

<400> 444
Gly Cys Cys Gly Ser Phe Ala Cys Arg Phe Gly Cys Val Xaa Cys Cys
1 5 10 15

Val

<210> 445
<211> 15
<212> PRT
<213> Conus textile

<400> 445
Cys Cys Ser Trp Asp Val Cys Asp His Pro Ser Cys Thr Cys Cys
1 5 10 15

<210> 446
<211> 16
<212> PRT
<213> Conus textile

<400> 446
Arg Cys Cys Lys Phe Pro Cys Pro Asp Ser Cys Arg Tyr Leu Cys Cys
1 5 10 15

<210> 447
<211> 17
<212> PRT
<213> Conus aureus

<400> 447
Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys Trp Pro Cys Cys Ile
1 5 10 15

Phe

<210> 448
<211> 16
<212> PRT
<213> Conus aureus

<400> 448
Cys Cys Asn Asp Trp Glu Cys Asp Asp Ser Cys Trp Pro Cys Cys Tyr
1 5 10 15

<210> 449
<211> 16
<212> PRT
<213> Conus ammiralis

<400> 449
Arg Cys Cys Arg Phe Pro Cys Pro Asp Thr Cys Arg His Leu Cys Cys
1 5 10 15

<210> 450
<211> 12
<212> PRT
<213> Conus ammiralis

<400> 450
Cys Cys Met Thr Cys Phe Gly Cys Thr Pro Cys Cys
1 5 10

<210> 451
<211> 18
<212> PRT
<213> Conus ammiralis

<400> 451
Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys Trp Pro Cys Cys Ile
1 5 10 15

Phe Ser

<210> 452
<211> 13
<212> PRT
<213> Conus ammiralis

<400> 452
Cys Cys Arg Leu Leu Cys Leu Ser Cys Asn Pro Cys Cys
1 5 10

<210> 453
<211> 16
<212> PRT

<213> Conus ammiralis

<400> 453
Cys Cys Asp Asp Ser Glu Cys Gly Tyr Ser Cys Trp Pro Cys Cys Tyr
1 5 10 15

<210> 454
<211> 16
<212> PRT
<213> Conus aulicus

<400> 454
Gly Cys Cys Ser Pro Pro Cys His Ser Ile Cys Ala Ala Phe Cys Cys
1 5 10 15

<210> 455
<211> 15
<212> PRT
<213> Conus aulicus

<400> 455
Cys Cys Arg Pro Val Ala Cys Ala Met Gly Cys Lys Pro Cys Cys
1 5 10 15

<210> 456
<211> 16
<212> PRT
<213> Conus aulicus

<400> 456
Glx Cys Cys Pro Ala Val Ala Cys Ala Met Gly Cys Glu Pro Cys Cys
1 5 10 15

<210> 457
<211> 18
<212> PRT
<213> Conus emaciatus

<400> 457
Cys Cys Ser Arg Asp Cys Ser Val Cys Ile Pro Cys Cys Pro Tyr Gly
1 5 10 15

Ser Pro

<210> 458
<211> 16
<212> PRT
<213> Conus episcopatus

<400> 458
Cys Cys Asp Glu Asp Glu Cys Asn Ser Ser Cys Trp Pro Cys Cys Trp
1 5 10 15

<210> 459
<211> 16
<212> PRT
<213> Conus episcopatus

<400> 459
Cys Cys Asp Glu Asp Glu Cys Ser Ser Ser Cys Trp Pro Cys Cys Trp
1 5 10 15

<210> 460
<211> 15
<212> PRT

<213> Conus episcopatus

<400> 460
Cys Cys Pro Ala Ala Ala Cys Ala Met Gly Cys Lys Pro Cys Cys
1 5 10 15

<210> 461
<211> 16
<212> PRT
<213> Conus omaria

<400> 461
Cys Cys Asp Glu Glu Glu Cys Ser Ser Ala Cys Trp Pro Cys Cys Trp
1 5 10 15

<210> 462
<211> 16
<212> PRT
<213> Conus omaria

<400> 462
Cys Cys His Leu Leu Ala Cys Arg Phe Gly Cys Ser Pro Cys Cys Trp
1 5 10 15

<210> 463
<211> 12
<212> PRT
<213> Conus spurius

<400> 463
Cys Cys Pro Arg Cys Ser Glu Cys Asn Pro Cys Cys
1 5 10

<210> 464
<211> 16
<212> PRT
<213> Conus pennaceus

<400> 464
Arg Cys Cys Lys Phe Pro Cys Pro Asp Ser Cys Lys Tyr Leu Cys Cys
1 5 10 15

<210> 465
<211> 19
<212> PRT
<213> Conus flavidus

<400> 465
Arg Cys Cys Arg Trp Pro Cys Pro Ser Ile Cys Gly Met Ala Arg Cys
1 5 10 15

Cys Ser Ser

<210> 466
<211> 14
<212> PRT
<213> Conus pulicarius

<400> 466
Cys Cys Lys Leu Leu Cys Gly Cys Thr Pro Cys Cys His Ile
1 5 10

<210> 467
<211> 15
<212> PRT

<213> Conus ebraceus

<400> 467
Cys Cys Glu Gln Pro Cys Tyr Met Gly Cys Ile Pro Cys Cys Phe
1 5 10 15

<210> 468
<211> 15
<212> PRT
<213> Conus ebraceus

<400> 468
Cys Cys Ala Gln Pro Cys Tyr Met Gly Cys Ile Pro Cys Cys Phe
1 5 10 15

<210> 469
<211> 14
<212> PRT
<213> Conus pulicarius

<400> 469
Cys Cys Val Ser Cys Tyr Met Gly Cys Ile Pro Cys Cys Phe
1 5 10

<210> 470
<211> 16
<212> PRT
<213> Conus miliaris

<400> 470
Cys Cys Asp Trp Pro Cys Ser Ala Gly Cys Tyr Pro Cys Cys Phe Pro
1 5 10 15

<210> 471
<211> 16
<212> PRT
<213> Conus miliaris

<400> 471
Gly Cys Cys Pro Pro Met Cys Thr Pro Cys Phe Pro Cys Cys Phe Arg
1 5 10 15

<210> 472
<211> 23
<212> PRT
<213> Conus rattus

<400> 472
Arg Gly Cys Cys Ala Pro Pro Arg Lys Cys Lys Asp Arg Ala Cys Lys
1 5 10 15

Pro Ala Arg Cys Cys Gly Pro
20

<210> 473
<211> 22
<212> PRT
<213> Conus stercusmuscarum

<400> 473
Glx Arg Cys Cys Asn Gly Arg Arg Gly Cys Ser Ser Arg Trp Cys Arg
1 5 10 15

Asp His Ser Arg Cys Cys
20

<210> 474
<211> 22
<212> PRT
<213> Conus consors

<400> 474
Gly Arg Cys Cys Asp Val Pro Asn Ala Cys Ser Gly Arg Trp Cys Arg
1 5 10 15

Asp His Ala Gln Cys Cys
20

<210> 475
<211> 23
<212> PRT
<213> Conus consors

<400> 475
Glx Arg Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys Ala Cys
1 5 10 15

Lys Ser Leu Lys Cys Cys Ser
20

<210> 476
<211> 22
<212> PRT
<213> Conus aurisiacus

<400> 476
Met Cys Cys Gly Glu Gly Arg Lys Cys Pro Ser Tyr Phe Arg Asn Ser
1 5 10 15

Gln Ile Cys His Cys Cys
20

<210> 477
<211> 19
<212> PRT
<213> Conus aurisiacus

<400> 477
Cys Cys Arg Trp Pro Cys Pro Arg Gln Ile Asp Gly Glu Tyr Cys Gly
1 5 10 15

Cys Cys Leu

<210> 478
<211> 22
<212> PRT
<213> Conus bullatus

<400> 478
Arg Cys Cys Gly Glu Gly Leu Thr Cys Pro Arg Tyr Trp Lys Asn Ser
1 5 10 15

Gln Ile Cys Ala Cys Cys
20

<210> 479
<211> 21
<212> PRT
<213> Conus caracteristicus

<400> 479

Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr Phe Arg Asp Asn Phe
1 5 10 15

Ile Cys Gly Cys Cys
20

<210> 480
<211> 23
<212> PRT
<213> Conus circumcisus

<400> 480
Arg Lys Cys Cys Gly Lys Asp Gly Pro Cys Pro Lys Tyr Phe Lys Asp
1 5 10 15

Asn Phe Ile Cys Gly Cys Cys
20

<210> 481
<211> 20
<212> PRT
<213> Conus ermineus

<400> 481
Cys Cys Ser Trp Pro Cys Pro Arg Tyr Ser Asn Gly Lys Leu Val Cys
1 5 10 15

Phe Cys Cys Leu
20

<210> 482
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Ile Cys Gly Cys Cys
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<211> 22
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<400> 483
Met Cys Cys Gly Glu Ser Ala Pro Cys Pro Ser Tyr Phe Arg Asn Ser
1 5 10 15

Gln Ile Cys His Cys Cys
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<210> 484
<211> 22
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Glx Lys Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr Phe Thr Asp
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Asn Phe Ile Cys Gly Cys
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<211> 23
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Glx Lys Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr Phe Arg Asp
1 5 10 15

Asn Phe Ile Cys Gly Cys Cys
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1 5 10 15

Asn Phe Ile Cys Gly Cys Cys
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Glx Lys Cys Cys Ser Gly Gly Ser Cys Pro Leu Tyr Phe Arg Asp Arg
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Leu Ile Cys Pro Cys Cys
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<400> 488
Glx Lys Cys Cys Gly Pro Gly Ala Ser Cys Pro Arg Tyr Phe Lys Asp
1 5 10 15

Asn Phe Ile Cys Gly Cys Cys
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Met Cys Cys Gly Glu Gly Ala Pro Cys Pro Ser Tyr Phe Arg Asn Ser
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Gln Ile Cys His Cys Cys
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<400> 490
Glx Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys Ala Cys
1 5 10 15

Lys Asn Leu Lys Cys Cys Ser
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<211> 23
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<400> 491
Glx Lys Cys Cys Thr Gly Arg Lys Gly Ser Cys Ser Gly Lys Ala Cys
1 5 10 15

Lys Asn Leu Lys Cys Cys Ser
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<210> 492
<211> 23
<212> PRT
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<400> 492
Val Thr Asp Arg Cys Cys Lys Gly Lys Arg Glu Cys Gly Arg Trp Cys
1 5 10 15

Arg Asp His Ser Arg Cys Cys
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<210> 493
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<212> PRT
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<400> 493
Val Gly Asp Arg Cys Cys Lys Gly Lys Arg Gly Cys Gly Arg Trp Cys
1 5 10 15

Arg Asp His Ser Arg Cys Cys
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<210> 494
<211> 24
<212> PRT
<213> Conus bullatus

<400> 494
Val Gly Glu Arg Cys Cys Lys Asn Gly Lys Arg Gly Cys Gly Arg Trp
1 5 10 15

Cys Arg Asp His Ser Arg Cys Cys
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<210> 495
<211> 26
<212> PRT
<213> Conus bullatus

<400> 495
Ile Val Asp Arg Cys Cys Asn Lys Gly Asn Gly Lys Arg Gly Cys Ser
1 5 10 15

Arg Trp Cys Arg Asp His Ser Arg Cys Cys

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<210> 496
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<212> PRT
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<400> 496
Val Gly Cys Cys Arg Pro Lys Pro Asn Gly Gln Met Met Cys Asp Arg
1 5 10 15

Trp Cys Glu Lys Asn Ser Arg Cys Cys
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<210> 497
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<400> 497
Arg Asp Cys Cys Thr Pro Pro Lys Lys Cys Lys Asp Arg Gln Cys Lys
1 5 10 15

Pro Gln Arg Cys Cys Ala
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<210> 498
<211> 23
<212> PRT
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<400> 498
Gly Arg Asp Cys Cys Thr Pro Pro Arg Lys Cys Arg Asp Arg Ala Cys
1 5 10 15

Lys Pro Gln Arg Cys Cys Gly
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<210> 499
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<212> PRT
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<400> 499
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1 5 10 15

Lys Pro His Arg Cys Cys
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<210> 500
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<400> 500
Arg Asp Cys Cys Thr Pro Pro Lys Lys Cys Arg Asp Arg Gln Cys Lys
1 5 10 15

Pro Ala Arg Cys Cys Gly
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<210> 501
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<213> Conus laterculatus

<400> 501
Arg Pro Pro Cys Cys Thr Tyr Asp Gly Ser Cys Leu Lys Glu Ser Cys
1 5 10 15

Met Arg Lys Ala Cys Cys
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<211> 22
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<400> 502
Arg Pro Pro Cys Cys Thr Tyr Asp Gly Ser Cys Leu Lys Glu Ser Cys
1 5 10 15

Lys Arg Lys Ala Cys Cys
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<223> Xaa is Hyp

<400> 503
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Xaa Gln Arg Cys Cys Ala
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Xaa Met Lys Cys Cys Ala
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Xaa Leu Lys Cys Cys Ala
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1 5 10 15

Lys Xaa His Arg Cys Cys
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<210> 507
<211> 22
<212> PRT
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<400> 507
Arg Asp Cys Cys Thr Pro Pro Lys Lys Cys Lys Asp Arg Gln Cys Lys
1 5 10 15

Pro Gln Arg Cys Cys Ala
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<210> 508
<211> 24
<212> PRT
<213> Conus marmoreus

<400> 508
Arg Gly Gly Cys Cys Thr Pro Pro Arg Lys Cys Lys Asp Arg Ala Cys
1 5 10 15

Lys Pro Ala Arg Cys Cys Gly Pro
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<210> 509
<211> 23
<212> PRT
<213> Conus nobilis

<400> 509
Glx Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys Ala Cys
1 5 10 15

Lys Asn Leu Lys Cys Cys Ser
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<210> 510
<211> 24
<212> PRT
<213> Conus parius

<400> 510
Arg Gly Gly Cys Cys Thr Pro Pro Lys Lys Cys Lys Asp Arg Ala Cys
1 5 10 15

Lys Pro Ala Arg Cys Cys Gly Pro
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<210> 511
<211> 23
<212> PRT
<213> Conus parius

<400> 511
Arg Gly Cys Cys Thr Pro Pro Arg Lys Cys Lys Asp Arg Ala Cys Lys
1 5 10 15

Pro Ala Arg Cys Cys Gly Pro
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<210> 512
<211> 24
<212> PRT
<213> Conus radiatus

<220>
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<222> (1)..(24)
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Leu Xaa Ser Cys Cys Ser Leu Asn Leu Arg Leu Cys Xaa Val Xaa Ala
1 5 10 15

Cys Lys Arg Asn Xaa Cys Cys Thr
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<211> 24
<212> PRT
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<220>
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<400> 513
Glx Gln Arg Cys Cys Thr Val Lys Arg Ile Cys Xaa Val Xaa Ala Cys
1 5 10 15

Arg Ser Lys Xaa Cys Cys Lys Ser
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<210> 514
<211> 24
<212> PRT
<213> Conus radiatus

<400> 514
Arg Gly Gly Cys Cys Thr Pro Pro Arg Lys Cys Lys Asp Arg Ala Cys
1 5 10 15

Lys Pro Ala Arg Cys Cys Gly Pro
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<210> 515
<211> 23
<212> PRT
<213> Conus stercusmuscarum

<400> 515
Glx Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys Ala Cys
1 5 10 15

Lys Asn Leu Lys Cys Cys Ser
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<210> 516
<211> 21
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<220>
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<222> (1)..(21)
<223> Xaa is Hyp

<400> 516
His Gly Cys Cys Lys Gly Xaa Glu Gly Cys Ser Ser Arg Glu Cys Arg
1 5 10 15

Xaa Gln His Cys Cys
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<210> 517
<211> 21
<212> PRT
<213> Conus tulipa

<400> 517
His Gly Cys Cys Glu Gly Pro Lys Gly Cys Ser Ser Arg Glu Cys Arg
1 5 10 15

Pro Gln His Cys Cys
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<210> 518
<211> 23
<212> PRT
<213> Conus wittigi

<400> 518
Leu Pro Ser Cys Cys Asp Phe Glu Arg Leu Cys Val Val Pro Ala Cys
1 5 10 15

Ile Arg His Gln Cys Cys Thr
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<210> 519
<211> 17
<212> PRT
<213> Conus omaria

<400> 519
Cys Cys Lys Tyr Gly Trp Thr Cys Leu Leu Gly Cys Thr Pro Cys Asp
1 5 10 15

Cys

<210> 520

<211> 17
<212> PRT
<213> Conus omaria

<400> 520
Cys Cys Arg Tyr Gly Trp Thr Cys Trp Leu Gly Cys Thr Pro Cys Gly
1 5 10 15

Cys